OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: October 1, 2003, 15:33:20 ; Search time 11456 seconds
(without alignments)
11612.963 Million cell updates/sec

Title: US-09-965-830-1_COPY_6_3257
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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17	869.8	26.7	3736	6	AR179196	AR179196 Sequence
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19	844.4	26.0	870	6	AR281268	AR281268 Sequence
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ALIGNMENTS

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LOCUS   AR179189   3323 bp   DNA   linear   PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6326168.
ACCESSION   AR179189
VERSION   AR179189.1 GI:20220744
KEYWORDS
SOURCE   Unknown.
  ORGANISM Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 3323)
  AUTHORS   Miyake,A., Mochizuki,S. and Yokoi,H.
  TITLE   Brain specific potassium channel protein
  JOURNAL   Patent: US 6326168-A 1 04-DEC-2001;
FEATURES   Location/Qualifiers

score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

Pred. No. is the number of results predicted by chance to have a

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                /organism="unknown"
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ORIGIN

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Best Local Similarity  100.0%;   Pred. No. 0:
Matches 3252;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0:
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Qy  301  CGGAAGAGGCGGGCGCTCCCGTCTCTGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA  360
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Qy  661  GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTC  720
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Qy 1921  AAGGGCGACCTGATCGGCTGTGAGCTGTAAAGGCCAATGCC  1980
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VERSION   AB022696.1 GI:5804783
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REFERENCE   1 (sites)
  AUTHORS   Miyake,A., Mochizuki,S., Yokoi,H., Kohda,M. and Furuichi,K.
  TITLE   New ether-a-go-go K(+) channel family members localized in human
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  JOURNAL   J. Biol. Chem. 274 (35), 25018-25025 (1999)
   MEDLINE   99386998
    PUBMED   10455180
REFERENCE   2 (bases 1 to 3610)
  AUTHORS   Miyake,A., Mochizuki,S., Yokoi,H., Kohda,M. and Furuichi,K.
  TITLE   Direct Submission
  JOURNAL   Submitted (21-JAN-1999) Akira Miyake, Yamanouchi Pharmaceutical
            Co.,Ltd., Molecular Medicine Laboratories; 21 Miyukigaoka, Tsukuba,
            Ibaraki 305-8585, Japan (E-mail:miyake@yamanouchi.co.jp,
            Tel:81-298-52-5111(ex.5324) Fax:81-298-52-5444)
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ORIGIN

Query Match   100.0%; Score 3252; DB 9; Length 3610;
Best Local Similarity 100.0%; Pred. No.0;
Matches 3252; Mismatches 0; Conservative 0; Indels 0; Gaps 0;
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Qy    2521  TTCCGGCTGTGGGCCAGTCTGGCCCCGGAATGTAGCAGCAGCCCTCCCTGACCAGAGAGC  2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2526  TTCCGGCTGTGGGCCAGTCTGGCCCCGGAATGTAGCAGCAGCCCTCCCTGACCAGAGAGC  2585

Qy    2581  GGCCTGCTCACTGTTCCCCATGGCCCCAGCGCAAGGAACACAGACACACTGGACAAG  2640
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Db    2586  GGCCTGCTCACTGTTCCCCATGGCCCCAGCGCAAGGAACACAGACACACTGGACAAG  2645

Qy    2641  CTTCGGCAGGCGGTGACAGAGCTGTCAGAGCTGCTCAGATCGCGGGAAGGACTGCAG  2700
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Db    2646  CTTCGGCAGGCGGTGACAGAGCTGTCAGAGCTGCTCAGATCGCGGGAAGGACTGCAG  2705

Qy    2701  TCACTTCGCCAGGCTGCAGCTTGTCTGCAGCTTGTCTGGCGCCCCACAGGGAGGGTCCGTGCCCCTCGG  2760
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Db    2706  TCACTTCGCCAGGCTGTGTCGCAGCTTGTCTGGCGCCCCACAGGGAGGGTCCGTGCCCCTCGG  2765

Qy    2761  GCATCGGGAGAGGGCCCGGCCCAGCAGCCACCTCCGGGCTTCTGCAGCCTCCGTGTGTG  2820
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Qy    2821  GACACTGGGGCATCCTCCTACTGCCTCGTCTGTCTTGAGTGGGACT  2880
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Qy    2881  TGGCCCACCCTGTCCCGGGCCTCCTCCCTCATGGCACCCTGGGCCTCCCCA  2940
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2886  TGGCCCACCCTGTCCCGGGCCTCCTCCCTCATGGCACCCTGGGCCTCCCCA  2945

Qy    2941  GCGTCTCAGAGCTCCCCCCTGGACCTCCGGGCCACCAGCGTTCTGGACCTCCACCTCAGACTCA  3000
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2946  GCGTCTCAGAGCTCCCCCCTGGCCTCCGAGCCACCAGCGTTCTGGACCTCCACCTCAGACTCA  3005

Qy    3001  GAGCCCCTCCTCTCGTCTCTGAGCCCAGCACCCCCTCCTCCCTGCTCCCCTCCTCCT  3060
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3006  GAGCCCCTCCTCTCGTCTCTGAGCCCAGCACCCCCTCCTCCCTGCTCCCCTCCTCCT  3065

Qy    3061  TCTGAGGAAGGGGCTAGGACTGGGGCCCCAGAGAGCTGTGAGGCTACCAGC  3120
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3066  TCTGAGGAAGGGGCTAGGACTGGGGCCCCAGAGAGCTGTGAGGCTACCAGC  3125

Qy    3121  ACTGGAGAGCCCCCACCAGGGTCAGGGGGCTGCGGGGCCTTGCCCTGGGACCCCACAGCCTG  3180
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Qy      1 ATGCGGGCCATGGGGGGCCTCCTGGGCGCCTCAGAACACCTTCCTCGGCACCATCCGCTACG    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     36 ATGCGGGCCATGGGGGGCCTCCTGGGCGCCTCAGAACACCTTCCTCGGCACCATCCGCTACG

Qy     61 CGGCTTCGACGGCGCACCACAGTAACTTCGTGCTGGGCCAACGCCCAGGTGGCGGGGCTCTC   120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     96 CGCTTCGACGGCGCACCACAGTAACTTCGTGCTGGGCCAACGCCCAGGTGGCGGGGCTCTC

Qy    121 CCCGGTGGTCTACTGCTCTGATGGCTTCGTGACCTTCTCCCGGGCTTCTGAGGTC          180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    181 ATGCAGGGGGCTGTGCTTCCTCCTCCTTTATGGGCCAGACACCAGTGAGCTCGTCCCG       240
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Qy    241 CAACAGATCCGCAAGGCCCTGGACGAGCAGGAGTTCAAGGCACAAGGAGTTCAAGGACTGA  300
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Db    276 CAACAGATCCGCAAGGCCCTGGACGAGCAGGAGTTCAAGGCACAAGGAGTTCAAGGACTGA

Qy    301 CGGAAGAGCGGGCTCCGTTCTCGGTGTCTTCCTGGATGTGATACCCATAAAGAATGAGAAA  360
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Qy    361 GGGGAGGTGGCTCTCTTCTCCAGTCTCTCCACAAGGACACATCAGCGGAAACCAAGAACCCGAGGG 420
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Db    396 GGGGAGGTGGCTCTCTTCTCCAGTCTCTCCACAAGGACACATCAGCGGAAACCAAGAACCGAGTG

Qy    421 GGCCCCGACAGAGTGGAAGGACAGTGGTGAGCACAGGTGGTGGCCCAAGCCAAGGAGTTGGTGTTTGGGGAGAAACCA 480
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Qy    481 AAAGGCTTCAATGCCAACCGGCGCGGCGAGCCCGTGCTCTCACCACCTGTCCGGGGGAC        540
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Qy    541 CTGCAGAAGCAGCCAAGGGCCAAGCTCAATAAGGGGGTGTTTGGGGAGAAACCA           600
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Qy    601 AACTTGCCTGAGTACAAAGTAGCCGGCCATCCGGAAGTCGGCCTTCATCCGTTGCACTCT        660
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Qy    661 GGGGCCACTGAGAGCCACCTGGGATGGCTTCCTCTTCATCCTCTATGTGGCTGCTC          720
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Qy    721 ACTGTGCCCTACAGGTGTGTGAGCACAGCAGGCACGCAGACCCCAGTGCCCGGCCCG        780
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Qy    781 CCCAGCGTCTGTGACCTGGCCTGGGAGTCCTCTTCATCCTGACATTGTGCTGAATTTC       840
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Qy    841 CGTACCACACATCTGTCCAAAGTCGGGGCCAGTTGGTGTGTTTGCCCCAAAGTCCATTTGCCTC   900
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Qy    901 CACTACGTCACCACCTGGTTCTCTGCGATGTCATCGGCCAGCGCTGCCCTTTGACCTGCTA     960
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Qy   1021 CGCCTGCTGCCCTGCCTGCCGACCGGTACTCGCAGTACGACGGCGCCGTGTGCTG          1080
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Qy   1081 ACACTGCTCATGGCCGTGTTCCCCCTGCGCTGCGGCCCACTGGGCGCCTGCTGGTTTTAC    1140
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Qy   1116 ACACTGCTCATGGCCGTGTTCCCCCTGCGCTGCGGCCCACTGGGCGCCTGGTTTTAC     1175
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Qy   1176 ATTGGCCAGGCAGGAGATCGAGAGCAGCAGCGAATCCGAGCTGCCGAGATTGGCTGGCTGCAG    1235
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Qy   1201 GAGCTGGCCCGCCCGACTGGAGAGACTCCTACTACTGGTGGCCGCACTGGAGGG     1260
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Qy   1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCTGCAGGGACGGGGGCTG     1320
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Qy   1321 GAGCTGCTGGGGCGGCCCCGTCGGCTGGGCTGGCCTTCGGCAACGGTTCCGGCCAACGCGCCTACATCACCTCCTACTTCCGCACTC    1380
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Qy   1621 CTGCAGAAGCAGCCAAGGGCCACAGCTCAATAAGGGGGTGTTTGGGGAGAAACCA     1680
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Qy   1681 AACTTGCCTGAGTCGTGTGTGAGCACAGCAGCCGCGCCATGTGCTACTGTGTTCATCCGAGCTGTTGCACTCT 1740
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Qy   1801 GGGGCCACTGAGAGCCACCTGGGATGGCTTCCTCTTCATCCTGACATTGTGCTGAATTTC  1860
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Qy   1921 AAGGGCGACCTGATCGGCTTGCAAGTCGGCGCTGATCGGCGTGAGCTGGTGAGCTGCCCCGG     1980
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Qy   1981 CACTACGTCACCACCTGGTTCTCTGCGATGTCATCGGCCAGCGCTGCCCTTTGACCTGCTA  2040
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Db   2136 AGCTACAACCTGGGTGCTGGGGACCGGTACTCGCAGAGTCGGGGAGCAGACCCCAGAGCGGC

Qy   2161 ACACTGCTCATGGCCGTGTTCCCCCTGCGCTGCGGCCCACTGGG-CGCCTGGTCTGGTTTTAC  2220
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RESULT 5

LOCUS   AB033108   3853 bp   mRNA   linear   PRI 11-NOV-1999
DEFINITION   Homo sapiens mRNA for KIAA1282 protein, partial cds.
ACCESSION   AB033108
VERSION   AB033108.1 GI:6331347
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (sites)
  AUTHORS   Nagase,T., Ishikawa,K., Kikuno,R., Hirosawa,M., Nomura,N. and
               Ohara,O.
  TITLE   Prediction of the coding sequences of unidentified human genes. XV.
               The complete sequences of 100 new cDNA clones from brain which code
               for large proteins in vitro
  JOURNAL   DNA Res. 6 (5), 337-345 (1999)
  MEDLINE   20039619
   PUBMED   10574462
REFERENCE   2 (bases 1 to 3853)
  AUTHORS   Ohara,O. Nagase,T. and Kikuno,R.
  TITLE   Direct Submission
  JOURNAL   Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,
               Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
               292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
               URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
               Fax:+81-438-52-3914)
FEATURES   Location/Qualifiers
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                     /db_xref="GI:6331348"
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                     PAGNSSGQSDNCSSSEANGTGLELLGGPSLRSAYITSLYFALSSLTSVGFGNVSAN
                     TDTEKIFSICTMLIGALMHAVVFGNVTAIIQRMYARRFLYHSRTRDLRDYIKIHRIPK
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ORIGIN

Db   2196 GACAATACCCTTATGTCCCACGTCTGGAGGAGGAAGGAGAGACAGATGGGAGCAGGGCCCACG 2255
Qy   2221 GTCTCCCCAGCCCAGCCTGATGAGACCCTCCAGCCCCTGCGTCCCCTGGCTGCACCTCC 2280
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Qy   2821 GACACTGGGGCATCCTCCTACTGCCTGCAGCCCCAGTGCTGCCTCTGTTCTTGAGCGGGACT 2880
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Qy   3121 ACTGGAGAGCCCCCACCAGGGCTCAGGGGCTCAGGGGCTGCCCTGCCCTGGGACCCCACCAGCCTG 3180
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Db   3156 ACTGGAGAGCCCCCACCAGGGCTCAGGGGCTCAGGGGCTGCCCTGCCCTGGGACCCCACAGCCTG 3215

Qy   3181 GAGATGTGGCTTATTGGCTGCCATGGCCTCCTGGCCAGTCCCAGTGGACCCCAGGAAGAAGGC 3240
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Db   3216 GAGATGTGGCTTATTGGCTGCCATGGCTGCCATGGCCTCCTGGCCAGTCCCAGTGGACCCCAGGAAGAAGGC 3275

Qy   3241 ACAGGGGTCTGA 3252
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Db   3276 ACAGGGGTCTGA 3287

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Query Match       100.0%;  Score 3250.4;  DB 9;  Length 3853;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 3251;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 0;

Qy      1 ATGCCGGCCATGCGGGGCCTCCTGGCGGCCTCAGAACACCTCCTGGACACCATCGCTACG      60
          ||||| ||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db   1281 CGGCTGCTGCGCCTGCTTCCGCGGCCTGCTCTGCCCGGCTGGGCTGCCGCTGGTGTGTTG    1340

Qy    261 ATGCGGGGCCTGCTGCCTGCGCTCCTTCCTTCCTTATGGCGGCAGCACCAGTGAGTCCGCCG     320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ACACTGCTACGCGGGGCCTCCGTGTCCGCCGTGCTCCGCCTGCTCCGCCGCACCATCGCTACG    1140

Qy     61 CGCTTCGACGGCACGCACCGCAACAGTAACTTCGTGCTGGCCAACGCCCAGTGGTGGGGGGCCTTC     120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341 ACACTGCTCATGGCCAGTGGTCGCCGTCTGCCTGCGCCCTCGCTGGGGCTGCCTGCTGTTTTAC    1400

Qy    321 CGCTTCGACGGCCACCGCAACAGTAACTTCGTGCTGGCCAACGCCCAGTGGTGGGGGGCCTTC     380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATTGGCCAGCGGGGAGATCGAGAGCAGCGAATCCGAGCTGCTGCGAGTCCGAGAGTTGGCTGCAG    1200

Qy    121 CCCGTGTGCTACTGCTTCTGTGATGACTTCGTCTCCCGGCTGCGAGGTC     180
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1491 ATTGGCCAGCGGGGAGATCGAGAGCAGCGAATCCGAGCTGCTGCGAGTCCGAGAGTTGGCTGCAG    1460

Qy    381 CCCGTGTGCTACTGCTGCTGTGATGACTTCGTCTCCCGGCTGCGAGGTC     440
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1202 GAGCTGGCCCGCGACTGGAGACTCCCTACTACCTGGTGGGCGGAGGCCAGCTGGAGGG    1260

Qy    181 ATGCAGCGGGGCCTGCTGCCTGCTCCTTCCTT·TATGGCGGCAGCACCAGTGAGTCCGCCG     240
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1461 GAGCTGGCCCGCGACTGGAGACTCCCTACTACCTGGTGGGCGGAGGCCAGCTGGAGGG    1520

Qy    441 ATGCAGCGGGGCCTGCTGCCTGCTCCTTCCTTCTTTATGGCGGCAGCACCAGTGAGTCCGCCG     500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AACAGCTCCGGCCCAGAGTGACAACTGCAGCAGCAGCCAACGCAGCGAGGCCAACGGACGGGGCTG    1320

Qy    241 CAACAGATACCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGAT·CCTGTAC     300
          ||||||||||||||||||||| |||||||||||||||||||||||| ||||||||
Db   1581 AACAGCTCCGGCCCAGAGTGACAACTGCAGCAGCAGCCAACGCAGCGAGGCCAACGGACGGGGCTG    1580

Qy    501 CAACAGATACCGCAAGGCCCTGGACGAGCACAACGAGTTCAAGGCTGAT·CCTGTAC     560
          ||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   1321 GAGCTGGCTGGGCGGCGCCCTCGCTGCGCGCCTCGCTACATCACCTCCTTACTTCGCACTC    1380

Qy    301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGCGTGTGCCGCCGATGTCATCGACGTCC     360
          ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   1641 GAGCTGGCTGGGCGGCGCCCTCGCTGCGCGCCTCGCTACATCACCTCCTTACTTCGCACTC    1640

Qy    561 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGCGTGTGCCGCCGATGTCATCGACGTCC     620
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Db   1381 AGCAGCTCACCAGCGTGGGGCTTCGGCAACGTGTCCCGCAACACGGACCACCGAGAAGATC    1440

Qy    361 GGGGAGGTGGCTCTCTCCAGTCTCTCACACAAGGAGTTCAGGACACCGAGAACCAGGAAAACCGAGGG     420
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Db   1701 AGCAGCTCACCAGCGTGGGGCTTCGGCAACGTGTCCCGCAACACGGACCACCGAGAAGATC    1700

Qy    621 GGGGAGGTGGCTCTCTCCAGTCTCTCACACAAGGAGTTCAGGACACCGAGAACCAGGAAAACCGAGGG     680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTCTCCATCTGCCACCATGCTCATCGGCGCGCCTGATGCTGCTGTGTTTGGAACGTG    1500

Qy    421 GGCCCCGACAGATGAAGGAGACAGGTGTGCCGGCCGTGCTGCCGCCGATGTGGCCGGCACGATCC     480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761 TTCTCCATCTGCCACCATGCTCATCGGCGCGCCTGATGCTGCTGTGTTTGGGAACGTG    1760

Qy    681 GGCCCCGACAGATGAAGGAGACAGGTGTGGCGGCCGTGCTGCCGCCGATGTGGCCGGCACGATCC     740
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Db   1501 ACGGCCATCATCCAGCGCATGCAGCGCATCCGTATCCCCAAGCCCGTATCCCCAGCAGCGGCGAC    1560

Qy    481 AAAGGGTTCAATGCCAACCGGGCGGCCGGGGCCGAGCGGGGCCGTGCTCTACCACCTGTCCGGGCAC     540
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Db   1821 ACGGCCATCATCCAGCGCATGCAGCGCATCCGTATCCCCAAGCCCGTATCCCCAGCAGCGGCGAC    1820

Qy    741 AAAGGGCTTCAATGCCAACCGGGCGGCCGGGGCCGAGCGGGGCCGTGCTCTACCACCTGTCCGGGCAC     800
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Db   1561 CTGCGGCGACTACATCCGCGCCATCGACGCCCCGTATCCCCAAGCCCCAAGCAGCGCATGCTGGAG    1620

Qy    541 CTGCAGAAGCAGCCCAAGGGCAAGAGCTACGCACACACAAGGGTGTTTGGGGAGAAACCA     600
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Db   1881 CTGCGGCGACTACATCCGCGCCATCGACGCCCCGTATCCCCAAGCCCCAAGCAGCGCATGCTGGAG    1880

Qy    801 CTGCAGAAGCAGCCCAAGGGCAAGAGCTACGCACACACAAGGGTGTTTGGGGAGAAACCA     860
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Db   1621 TACTTCCAGGCACTGGGCGTGAACAATGGCATGGCGGTGCTGCGAGCTGCGAGAGC    1680

Qy    601 AACTTGCCTGAGTAGTACAAAGTAGCCGCCATCGGGAAGTCGCCCTCTGTTGCACTGT     660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941 TACTTCCAGGCACTGGGCGTGAACAATGGCATGGCGGTGCTGCGAGCTGCGAGAGC    1940

Qy    861 AACTTGCCTGAGTAGTACAAAGTAGCCGCCATCGGGAAGTCGCCCTCTGTTGCACTGT     920
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Db   1681 CTCCCTGACGAGCTGCGCGACGCGCGCCAGCATCGCCATGCACCTGCACAAGGAGCTGCCTCCAGCTGT    1740

Qy    661 GGGGCACTGAGAGCCACCTGGATGGCTTCATCCTGCTCGCGCCGCACTCGGTTCATTGCCTC     720
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Db   2001 CTCCCTGACGAGCTGCGCGACGCGCGCCAGCATCGCCATGCACCTGCACAAGGAGCTGCCTCCAGCTGT    2000

Qy    921 GGGGCACTGAGAGCCACCTGGATGGCTTCATCCTGCTCGCGCCGCACTCGGTTCATTGCCTC     980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CCACTGTTTGAGGCGGCCAGCGGCGGCGGCTGTCTCCGGCGCCGCCTGCGGCCCGGCCC    1800

Qy    721 ACTGTGCCCTACAGCGCGTGTGTGAGCAGCCGTCATCGCAGCACGGCGCCAGTCCCGCCCCG     780
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Db   2061 CCACTGTTTGAGGCGGCCAGCGGCGGCGGCTGTCTCCGGCGCCGCCTGCGGCCCGGCCC    2060

Qy    981 ACTGTGCCCTACAGCGCGTGTGTGAGCAGCCGTCATCGCAGCACGGCGCCAGTGCCCGCCCCG    1040
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Db   1801 GCCTTCTGCACGCACTGGCGGAGCTGCGCGCAGATCGCCATGCACGCCGGCGGGCCCCTCTAC    1860

Qy    781 CCCAGGCGTCTG·GACCTGGCCCTGAGGTCCCTTCATCCTTGACAIGTGC·GAATTC     840
          ||||||||||| |||||||||||||||||||||||||||||| |||||| |||||
Db   2121 GCCTTCTGCACGCACTGGCGGAGCTGCGCGCAGATCGCCATGCACGCCGGCGGGCCCCTCTAC    2120

Qy   1041 CCCAGGCGTCTGTGACCTGGCCCTGGAGGTCCCTTCATCCTTGACAAGTGCTGAATTTC    1100
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Db   1861 TTTGTCTGCTCGGCCTCCATGCAGGTGCTTCAAGGTGGCTCAGGTGCTGCGAGGG    1920

Qy    841 CGTACCACATTCGTGTCCAAGTCCGGGCAAGCGTGTTGCCCCAAAGTCCATTTGCCTC     900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 AAGGGCGACTGATCGGTCGTGAGCTGGAGCTGCGGCCCCGGCAGTGGCAGCAGTGGTAAAGGCCAATGCC    1980

Qy   1101 CGTACCACATTCGTGTCCAAGTCCGGGCAAGCGTGTTGCCCCAAAGTCCATTTGCCTC    1160
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Db   2181 AAGGGCGACTGATCGGTCGTGAGCTGGAGCTGCGGCCCCGGCAGTGGCAGCAGTGGTAAAGGCCAATGCC    2240

Qy    901 CACTACGTCACCACCTGGTTCCTGCTGGATGTCATCGCAGCGCGCCCTCTTGACCTGCTA     960
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Db   1981 GACGTGAAGGGCGTGACGTACTGCGTCCTGCAGTGTCTGCACGCGGACTGAGGTC    2040

Qy   1161 CACTACGTCACCACCTGGTTCCTGCTGGATGTCATCGCAGCGCGCCCTTTGACCTGCTA    1220
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Db   2241 GACGTGAAGGGCGTGACGTACTGCGTCCTGCAGTGTCTGCACGCGGACTGAGGTC    2300

Qy    961 CATGCCTTCAAGGTCAACCTGTCACTTCGGGGCTCAACGTCAACGGTCCATCGGGGC    1020
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Db   1221 CATGCCTTCAAGGTCAACCTGTCACTCGACTTCGGGGCCCATCTGCTCAAGAGCAGTCCCAGTGGGAGCTC    1280

Qy   1021 CGGCTGCTGCGCCTGCTTCCGCGGCCTGCTCTGCCCGGCTACTGCGGTCGCTGGTGCTG    1080
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Db   2101 AGCTACAACCTGGTCGTGCTGGGGAGGCTCTGCAGAGGTGGACACCAGCTCCCTGAGCGGGC    2160
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Db   3241 ACAGGGCTCTGA 3252
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Qy   3501 ACAGGGTCTGA 3512
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RESULT 4
AR217183
LOCUS        AR217183                    3249 bp    DNA      linear    PAT 25-SEP-2002
DEFINITION   Sequence 2 from patent US 6413741.
ACCESSION    AR217183
VERSION      AR217183.1  GI:23316610
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1 (bases 1 to 3249)
  AUTHORS    Jegla,T.J. and Wickenden,A.
  TITLE      Human elk a voltage-gated potassium channel subunit
  JOURNAL    Patent: US 6413741-A 2 02-JUL-2002;
FEATURES             Location/Qualifiers
     source          1..3249
                     /organism="unknown"
BASE COUNT     562 a   1097 c   1000 g    590 t
ORIGIN
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Query Match   99.8%;   Score 3245.8;   DB 6;   Length 3249;
Best Local Similarity 99.9%;   Pred. NO. 0;
Matches 3247;   Mismatches 0;   Conservative 0;   Indels 2;   Gaps 0;

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Qy      1 ATGCCGCCATGCGGGGCCTCTGGCGCCTCAGAACACTTCTGGACACCATCGCTACG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGCCGCCATGCGGGGCCTCCTGGCGCCCAGAACACTTCCTGGACACCATCGCTACG 60

Qy     61 CGCTTCGACGCGCACGCACAGTAACTTCGTGCTGGCAACGCCCAGTGCGCGGGGGCTCTTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CGCTTCGACGCGCACGCACAGTAACTTCGTGCTGGCAACGCCCAGTGCGCGGGGGCTCTTC 120

Qy    121 CCCGTGGTCTCTACTGCTTCGTGATGGCTTCTGTGACCTCCACGGGGCTTCTCCCGGGTGAGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCGTGGTCTCTACTGCTTCGTGATGGCTTCTGTGACCTCCACGGGGCTTCTCCCGGGTGAGTC 180

Qy    181 ATGCAGCGGGGCGTGTGCCTGCCTCCTTCCTTATGGGCACAAGGAGTCGAGCTGAGCTGCTCGCGC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATGCAGCGGGGCGTGTGCCTGCCTGCCTCCTTCCTTATGGGCACAAGGAGTCGAGCTGAGCTGCTCGCGC 240

Qy    241 CAACAGATCCGCAAGGCCCTGACGAGCACAAGGAGTTCAAGGTCATCCTGTAC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAACAGATCCGCAAGGCCCTGACGAGCACAAGGAGTTCAAGGTCGTGATCCTGTAC 300

Qy    301 CGGGAGGAGCCGGCGTCCCGTTCCTCCTCTCACAGACTCGGGCTCCCCA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 CGGGAGGAGCCGGCGTCCCGTTCCTCCTCTCACAGACTCGGGCTCCCCA 360

Qy    361 GGGGAGGTGGCTCTCTCCAGTCTCTCAGTCCTCAGACTCA 420
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGGGAGGTGGCTCTCTCCAGTCTCTCAGTCCTCAGACTCA 420

Qy    421 GGCCCCGACAGATGGAAGGAGCAGTGGTGGCCGGCCGACGATCC 480
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Db    421 GGCCCCGACAGATGGAAGGAGCAGTGGTGGCCGGCCGACGATCC 480

Qy    481 AAAGGCTTCAATGCAACCGGCGGAGGGCTACCAGC 540
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Db    481 AAAGGCTTCAATGCAACCGGCGGAGGGCTACCAGC 540

Qy    541 CTGCAGAAGCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 600
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Db    541 CTGCAGAAGCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGAGAAACCA 600

Qy    601 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT 660
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Db    601 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT 660
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Db   2220 AGCTACAAACTGGGTGCTGGGGGAGGGCTCTCGCAGAGGTGGACACCAGGTCCCTGAGCGGC 2220
Qy   2161 GACAATACCCTTATGTCCACGCTGGGGAGGAGACAGATGGGGAGGAGCAGGGCCCCACG 2220
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   2421 GACAATACCCTTATGTCCACGCTGGGGAGGAGACAGATGGGGAGGAGCAGGGCCCCACG 2480

Qy   2221 GTCTCCCCAGCCCCAGCTGATGAGCCCCCAGCGCCCTCGTGTCCCTGCTGCACCTC 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2481 GTCTCCCCAGCCCCAGCTGATGAGCCCCCAGCGCCCTCGTGTCCCTGCTGCACCTCC 2540

Qy   2281 TCATCCTCAGCTGCCAAGCTGTATCCCCACGTCGTCGAACAGCACCTCGTCTAGGT 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2541 TCATCCTCAGCTGCCAAGCTGTATCCCCACGTCGTCGAACAGCACCTCGTCTAGGT 2600

Qy   2341 GGCAGAGGGAGGCCAGGCAGGCCAGGGGCAGGGGCTTTGAAGGCTGAAGGCTGGGGCTGGCCCCTCTGCCCCC 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2601 GGCAGAGGGAGGCCAGGCAGGCCAGGGGCAGGGGCTTTGAAGGCTGAAGGCTGGGGCTGGCCCCTCTGCCCCC 2660

Qy   2401 CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCCATGCGTCGATGAATGTGCCCCCAGATCTG 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2661 CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCCATGCCATGGAATGTGCCCCCAGATCTG 2720

Qy   2461 AGCCCAGGGTAGTAGATGGCATTGAAGACGGTGTGGCTCGGACCCAAGTTCTCT 2520
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2721 AGCCCAGGGTAGTAGATGGCATTGAAGACGGTGTGGCTCGGACCCAAGTTCTCT 2780

Qy   2521 TTCCGGCGTGGCCAGTCTGCCCGGAATGTAGCAGCACAGCCCCCTGCCCCCTGACCAGAGAGC 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2781 TTCCGGCGTGGCCAGTCTGCCCGGAATGTAGCAGCACAGCCCCCTGCCCCCTGACCAGAGAGC 2840

Qy   2581 GGCCTGCTCACTGTTCCCCATGGGCCCAGCGAGGCAAGGACACTGGACAAG 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2841 GGCCTGCTCACTGTTCCCCATGGGCCCAGCGAGGCAAGGACACTGGACAAG 2900

Qy   2641 CTTCGGCAGGGGTGACAGAGCTGTCAGATGCGGAAGGACTGCAG 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2901 CTTCGGCAGGGGTGACAGAGCTGTCAGATGCGGAAGGACTGCAG 2960

Qy   2701 TCACTTCGCCAGGCTGTGCAGCTTGTCTCGGCGCCCACAGGAGGGGTCCGTGCCCCTCGG 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2961 TCACTTCGCCAGGCTGTGCAGCTTGTCTCGGCGCCCACAGGAGGGGTCCGTGCCCCTCGG 3020

Qy   2761 GCATCGGGAGAGGGGGGCCTGCCCAGCAGCCTCCGGCTTCTGCAGCCTCTGTGTGG 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3021 GCATCGGGAGAGGGGGGCCTGCCCAGCAGCCTCCGGCTTCTGCAGCCTCTGTGTGG 3080

Qy   2821 GACACTGGGGCATCCTCTACTGCCTGCCTGGCTTGTCTTGAGTGGGACT 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3081 GACACTGGGGCATCCTCTACTGCCTGCCTGGCTTGTCTTGAGTGGGACT 3140

Qy   2881 TGGGCCCCACCCGTCGCGGGGCATCCTCCTCCGGCTCCCCACCTGGGGTCCCCCA 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3141 TGGGCCCCACCCGTCGCGGGGCATCCTCCTCCGGCTCCCCACCTGGGGTCCCCCA 3200

Qy   2941 GCGTCTTCAGAGCTCGGGCCCGGACCTTCTGGACCTCCACCTCAGACTCA 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3201 GCGTCTTCAGAGCTCGGGCCCGGACCTTCTGGACCTCCACCTCAGACTCA 3260

Qy   3001 GAGCCCCCTGCCTCTGCTCTGAGCAGCTGCTTGCTCTGGCCACCGGCGTCTGAGGCTACCAGC 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3261 GAGCCCCCTGCCTCTGCTCTGAGCAGCTGCTTGCTCTGGCCACCGGCGTCTGAGGCTACCAGC 3320

Qy   3061 TCTGAGGAAGGGCTAGGACTGGGCCCCAGAGGCTGTGAGGCTACCAGC 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3321 TCTGAGGAAGGGCTAGGACTGGGCCCCAGAGGCTGTGAGGCTACCAGC 3380

Qy   3121 ACTGGAGAGCCCCCACCAGGGTCACGGGGCTCAGGGGACCCTGCCTGCCTTGGGAGGACGACCTG 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3381 ACTGGAGAGCCCCCACCAGGGTCACGGGGCTCAGGGGACCCTGCCTGCCTTGGGAGGACGACCTG 3440

Qy   3181 GAGATGCTGCTTATTGGCTGCCATGGCTCTCGGCACAGTCCAGTGCAGTCAGAAGAGGC 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3441 GAGATGCTGCTTATTGGCTGCCATGGCTCTCGGCACAGTCCAGTGCAGTCAGAAGAGGC 3500
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This page consists of a two-column DNA sequence alignment (rotated 90°). Each alignment block contains a query line (Qy) and a database line (Db) with match bars between them, labeled by nucleotide position numbers.

Right column (Qy / Db), positions:
1741, 1801, 1861, 1921, 1981, 2041, 2101, 2161, 2221, 2281, 2341, 2401, 2461, 2521, 2581, 2641, 2701, 2761, 2821 ending at 1800/1800, 1860/1860, 1920/1920, 1980/1980, 2040/2040, 2100/2100, 2160/2160, 2220/2220, 2280/2280, 2340/2340, 2400/2400, 2460/2460, 2520/2520, 2580/2580, 2640/2640, 2700/2700, 2760/2760, 2820/2820, 2880.

Left column (Qy / Db), positions:
661, 721, 781, 841, 901, 961, 1021, 1081, 1141, 1201, 1261, 1321, 1381, 1441, 1501, 1561, 1621, 1681 ending at 720, 780, 840, 900, 960, 1020, 1080, 1140, 1200, 1260, 1320, 1380, 1440, 1500, 1560, 1620, 1680, 1740.

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                                                             GPESGLLTVPHGPSEARNTDILDKLRQAVTELSEQVLQMREGLQSLRQAVQLVLAPHR
Db  2821  |||||||||||||||||||||||||||||||||||||||||||||||| ||    ||
          GACACTGGGCATCCTCCTACTGCCTCCCAGCCTCGCCTGCTCTTGAGTGGGGACT 2880  EGPCPRASGEGPCPASTSGLLQPLCLDTGASSYCLQPPAGSVLSGTWPHRPGPPLM

Qy  2881  TGGCCCCACCCTCGTCCGGGGCCTCCTCCCCCATGGCACCCTGGCCCTGGGGTCCCCCA 2940  APWPWGPPASQSSPWPRATAFWTSTSDSEPPASQDLCSEPSTPASPPPSEEGARTGPA
Db  2881  TGGCCCCACCCTCGTCCGGGGCCTCCTCCCCCATGGCACCCTGGCCCTGGGGTCCCCCA 2940  EPVSQAEATSTGEPPPGSGGALPWDPHSLEMVLIGHGSGTVQWTQEEGTGV*

Qy  2941  GCGCTCTCAGAGCTCCCCTGCCTCGGAGCCACAGCTTCTCCACCTCAGATCA 3000
Db  2941  GCGCTCTCAGAGCTCCCCTGCCTCGGAGCCACAGCTTCTCCACCTCAGACTCA 3000

Qy  3001  GAGCCCCTGCCTCAGGAGACCTCTGTCTGAGCCCAGCCCAGCCAGGCTGTCGTAACG 3060
Db  3001  GAGCCCCTGCCTCAGGAGACCTCTGTCTGAGCCCAGCCCAGCCAGGCTGTCGTAACG 3060

Qy  3061  TCTGAGGAGGGGCTAGGACTGGGCCCCGAGAGCCTGAGCCAGCCTGAGGCTACCAGC 3120
Db  3061  TCTGAGGAGGGGCTAGGACTGGGCCCCGAGAGCCTGAGCCAGCCTGAGGCTACCAGC 3120

Qy  3121  ACTGGAGAGCCCCCACCAGGGTCAGGGGGCTTGCCCTGGGACCCCACAGCCTG 3180
Db  3121  ACTGGAGAGCCCCCACCAGGGTCAGGGGGCTTGCCCTGGGACCCCACAGCCTG 3180

Qy  3181  GAGATGGTGCTTATTGGCTGCCATGGCTCTCGGCACAGTCCAGTCCAGGAGAAGAGGC 3240
Db  3181  GAGATGGTGCTTATTGGCTGCCATGGCTCTCGGCACAGTCCAGTCCAGGAGAAGAGGC 3240

Qy  3241  ACAGGGTC 3249
Db  3241  ACAGGGTC 3249
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```
BASE COUNT    562 a    1099 c    1000 g    591 t
ORIGIN

Query Match      99.88;  Score 3244;  DB 6;  Length 3252;
Best Local Similarity  99.88%;  Pred. No. 0;
Matches 3247;  Conservative  0;  Mismatches  0;  Indels  5;  Gaps  0;
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Qy    1  ATGCCGGCCATGCGGGGCCTCCTGGCCCTCAGAACACTTCCTGCACACCTCGCTACG  60
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Db    1  ATGCCGGCCATGCGGGGCCTCCTGGCCCTCAGAACACTTCCTGCACACCTCGCTACG  60

Qy   61  CGCTTCGACGGCACGCACGACTAACTTCGTCTGGCAACGCTCACGGCTTCTCCGGGGCTCTTC  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  CGCTTCGACGGCACGCACGTACTCTGTCTGGCAACGCTCACGGCTTCTCCGGGGCTCTTC  120

Qy  121  CCCGTGGTCTACTGCTCTCATGGCTTCTCGTTCTTATGGCTCCTTATGGGCCACCAGTCC  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  CCCGTGGTCTACTGCTCTCATGGCTTCTCGTTCTTATGGCTCCTTATGGGCCACCAGTCC  180

Qy  181  ATGCAGCGGGGCGTGCCTGCCTGGCACAGTCCAGTCCAGTCCAGGAGAAGAAGGC  240
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Db  241  CAACAGATCCGCAAGGCCCTGGACGCACCCGGGTCCCGTCTCTGGTGATGTGATACCCATAAAGATATGAGAAA  300

Qy  301  CGGAAGAGCGGGCTCCCGTCTGTCCGATGTGTCTCTCGGTGTCTCCGGATGTGATACCCATAAAGATATGAGAAA  360
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Qy  421  GGCCCGACAGATGGAAGGAGACAGGTGGTGGCCGCGGCGCGCGATATGGCCGGGCACGATCC  480
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Qy  481  AAAGGCCACTCAATGCCAAGGGCACGGGGTCGCCTTCATCCGTTGCACTGTTGGCTGGCTGTGTCGGCGGCAC  540
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Db  481  AAAGGCCTTCAATGCCAAGGGCACGGGGTCGCCTTCATCCGTTGCACTGTTCACCACCTGTCCGGGCAC  540

Qy  541  CTGCAGAAGCAGCCCAAGGCCAAGCAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA  600
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Db  541  CTGCAGAAGCAGCCCAAGGCCAAGCAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA  600

Qy  601  AACTTGCCTGAGTACAAAGTAGCCCCATCCGGAAGTCGCCCTTCATCCGTTGCACTGT  660
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Qy  661  GGGGCACTGAGAGCCACTGGGATGGCTTCATCCTGCTCAGCAGCAGGAGCCCAGGTGCGCGGCCCG  720
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Qy  781  CCCAGGCGTCTGTGACCGGCGTGACTACCTGGGAGGTCCTTGACATTGTGCTGGAATTTC  840
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Qy  841  CGTACCACATTCGTGTCCAAGTCGGGCACGTGGTTGCCCAAAGTCCATTTGCCTC  900
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Db  841  CGTACCACATTCGTGTCCAAGTCGGGCACGTGGTTGCCCAAAGTCCATTTGCCTC  900

Qy  901  CACTACGTTCACCCACCTGGTTCCTGCTGGATGTCATCGCAGCCGACCTGCTA  960
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RESULT 5
AX027893
LOCUS       AX027893          3252 bp    DNA    linear    PAT 15-SEP-2000
DEFINITION  Sequence 1 from Patent EP1002863.
ACCESSION   AX027893
VERSION     AX027893.1    GI:10188725
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Avenet,P. and Renard,S.
  TITLE     A potassium channel member of the erg family
  JOURNAL   Patent: EP 1002863-A 1 24-MAY-2000;
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FEATURES             Location/Qualifiers
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                     VSPAPADEPSSPLLSPGCTSSSSAAKLLSPRRTAPRPRLGGRGPGRAGALKAEAGPS
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Db   901 CACTACGTCACCACCTGGTTCCTGCTGGATGTCATCGGCGCGTGCCTTGACCTGCTA  960
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Qy   961 CATGCCTTCAAGGTCAACGTGACTTCGGGGGCCCATCTGCTGAAGACGTGCCGCCTGCTG 1020
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Db   961 CATGCCTTCAAGGTCAACGTGACTTCGGGGGCCCATCTGCTGAAGACGTGCCGCCTGCTG 1020

Qy  1021 CGCTGCTGCGCGGCCTGCTTCCGCGGGCTACTCCGGCCAGTACACGGCCGTGTGGTGCTG 1080
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Qy  1141 ATTGGCCAGGGAGATCGAGAGCAGCGAATCCGAGTTGCCTGAGATTGGCTGGCTGCAG 1200
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Db  1201 GAGCTGGCCGCCCCGGACTGGAGACTCCCTACTACCTGGTCGGCGGAGGCCGAGCTGGAGGG 1260

Qy  1261 AACAGCTCCGGCCCAGAGTGACAACTGCAGCAGCGAATCGCAGGCCAACGGCAGGGGCTG 1320
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Qy  1321 GAGCTGCTGGGGCGGCCGTGCCTGTGCGGCAGCCCTACATCACCTCCCTCTCTACTTCGCACTC 1380
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Db  1321 GAGCTGCTGGGGCGGCCGTGCCTGTGCGGCAGCCCTACATCACCTCCCTCTCTACTTCGCACTC 1380

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Db  1501 ACGGCCATCATCAGCGACTACTCACCGCGCGGCCATGTACGCCCCGCTTCTGTACCACAGCCCCGCAC 1560

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Qy  1621 TACTTCCAGGCCACCTGGGCGGTGAACAATGGCATCACCACCAAGGCATGCTGCTGCAGAGC 1680
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Qy  1681 CTCCCTGACGAGCTGCGCGCCAGCATCGCGCCGCCATGCACCTGCACAAGAGGTCCTGCAGCTG 1740
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Qy  1741 CCACTGTTTGAGGCGGCCAGCGGCCACTGTCTCTGCGGGCACTGGGGTCCCCGGGCCC 1800
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Qy  1801 GCCTTCTGCACGCGCGGCGAGTACTCATCACCACCAAGGCGATGGTGGCACCGTCAAGGGTCAAGGGG 1860
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Db  1801 GCCTTCTGCACGCGCGGCGAGTACTCATCACCACCAAGGCGATGGTGGCACCGTCAAGGGTCAAGGGG 1860

Qy  1861 TTTGTGCTCTGGCTGCTCCATGGAGGTGCGGCCACCGTGTCAAGGGTGTAAAGCCCATCCTAGGG 1920
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Qy  1921 AAGGGCCACCTGATCGGCTGCGGCGGCCGCGGAGCAGGTGCCAATGCCCGAGGCCAATGCCC 1980
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Db  1921 AAGGGGACCTGATCGGCTGCGGCGGCCGCGGAGCAGGTGCCAATGCCCGAGGCCAATGCCC 1980

Qy  1981 GACGTGAAGGGGCTGACGTACTGCCTGCTCCAGTTGCTCTGCAGTTGCTGCTGCCTGCTGGCCTGCAGC 2040
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Db  1981 TCTGAGGAAGGGGCTGACGTACTAGGACTGCCCCCAGAGACCGCTGTGAGGCTACCAGGCTGGCCTGCAGC 2040
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Qy  2041 AGCCTTGCGCGTGCACCCGAGTTGCCCGCGCCTTCGCGCCGCTTCCGAGGGGAGCTC 2100
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Qy  2161 GACAATACCCTTATGTCCACGCTGGAGGAGGAGGAGCAGATGGGAGCAGGGCCCCACG 2220
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Db  2161 GACAATACCCTTATGTCCACGCTGGAGGAGGAGGAGCAGATGGGAGCAGGGCCCCACG 2220

Qy  2221 GTCTCCCCACCCCAGCTCATGAGCCCTCCAGCCCCCTGTCCCCTGGCTGTCCCTGCACCTCC 2280
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Db  2221 GTCTCCCCACCCCAGCTGATGAGCCCTCCAGCCCCTGTCCCCTGGCTGTCCCTGCACCTCC 2280

Qy  2281 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGCACCACCGTCGTCGTCTAGG 2340
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Qy  2881 TGGCCCCACCCTCGTCCGGGGGCCTCCTCCCTCGCGGGCCACAGCTTTCTGGACCCCCCA 2940
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Qy  2941 GCGTCTCAGAGCTCGTCTGGCCTCGAGGCCACCTCAGCCTCCAGGG 3000
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Qy  3121 ACTGGAGAGCCCCACCAGGGTCAGGGGCCTGSCCTGCCCTGGGACCCCACAGCCTG 3180
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Qy  3241 ACAGGGGTCTGA 3252
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Db  3241 ACAGGGGTCTGA 3252

RESULT 6
AR212361
LOCUS       AR212361          3857 bp    DNA          linear     PAT  20-JUN-2002
DEFINITION  Sequence 19 from patent US 6399761.
ACCESSION   AR212361
VERSION     AR212361.1  GI:21515915
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 3857)
  AUTHORS   Miller,A.P., Hu,P., Curran,M.Edward., Rutter,M. and Jiang-Yang.W.
  TITLE     Nucleic acid encoding human potassium channel K+ novi protein
  JOURNAL   Patent: US 6399761-A 19 04-JUN-2002;
FEATURES             Location/Qualifiers
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BASE COUNT      677 a   1301 c   1201 g    678 t
ORIGIN

Query Match        99.0%;   Score 3218;   DB 6;   Length 3857;
Best Local Similarity   99.8%;   Pred. No. 0;
Matches 3244;  Conservative   0;  Mismatches   0;  Indels   3;  Gaps   2;

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Qy    61 CGCTTCGACGGCACGCACGCACCAGTAACTTCGTGCTGGACGCCAAGCGCCAGTGGGGGCTTC  120
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Db   309 CGCTTCGACGGCACGCACGCACCAGTAACTTCGTGCTGCGGGCAACGCC--AGTGGGGGGCTCT-  365

Qy   121 CCCGTGTCTACTGCTGTGTGATGGCTTCTTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC  180
         ||| |||||||||||||||||||||||||||||||||||| ||||||||||
Db   366 CCCTGGGTCTACTGCTGTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC  425

Qy   181 ATGCAGCGGCGGCTGTGCCTGCTCCTTCCTTATGGGCACACACCAGTGACTGAGCTGTCCGG  240
         ||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   426 ATGCACGCGGCGGCGTGCCTGCTCCTTCCTTATGGGCACACACCAGTGAGCTCGTGTCGGCTG  485

Qy   241 CAACAGATCCGCAAGGCGGGCTCCCGTTCTGGACGAGGCACAAGGAGTTCAAGGCTGAGCTGAT  300
         ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   486 CAACAGATCCGCAAGGCGGGCTCCCGTTCTGGACGAGGCACAAGGAGTTCAAGGCTGAGCTGAT  545

Qy   301 CGGAAGAGCGGGCTCCCGTTCGGGCGTCCTGGGTGTCCTGATGTGATACCCATAAAGAATGAGAAA  360
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Db   546 CGGAAGAGCGGGCTCCCGTTCGGGCGTCCTGGGTGTCCTGATGTGATACCCATAAAGAATGAGAAA  605

Qy   361 GGGGAGGTGGCTCTCTTCCTAGTCTCTCACAGGACATCAGCGAAACCAAGAACCGAGGG  420
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Db   606 GGGGAGGTGGCTCTCTTCCTAGTCTCTCACAGGACATCAGCGAAACCAAGAACCGAGGG  665

Qy   421 GGCCCCGACAGATGGAAGGAGCACAGGTGGTGGCGGCCCGATATGGCCGGGCACGGATCC  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   666 GGCCCCGACAGATGGAAGGAGCACAGGTGGTGGCGGCCCGATATGGCCGGGCACGGATCC  725

Qy   481 AAAGGCTTCAATGCCAACTGCCAACTGGCGTCCTTCTACCACCTGTCTCCGGGCAC  540
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Db   726 AAAGGCTTCAATGCCAACTGCCAACTGGCGTCCTTCTACCACCTGTCTCCGGGCAC  785
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Db  2946 TCACTTCGCCAGGCTGTGCAGCTTGTCCTGCGGCGCCCCACAGGAGGGTCCGTGCCCTCGG 3005
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Qy  2761 GCATCGGGAGAGGGGCCGTGCCCAGCCAGCCACCTGCAGCCTCCTGCAGCCTCGTGTGTG 2820
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3006 GCATCGGGAGAGGGGCCGTGCCCAGCCAGCCACCTGCAGCCTCCTGCAGCCTCGTGTGTG 3065
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Qy  2821 GACACTGGGCATCCTCCTACTGCCTGAGCCCCAGCGTTGGCTCTGTCTTGAGTGGGACT 2880
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Db  3126 TGGCCCCACCCTCGTCCGGGGCCTCCTCCCCATGGCACCCCGGCCCTGGGGTCCCCA 3185
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Qy  2941 GCGTCTCAGAGCTCCCCCTGGCCTTCGAGCCACAGCGTTTCTGGACCTCCACCTCAGACTCA 3000
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Db  3186 GCGTCTCAGAGCTCCCCCTGGCCTTCGAGCCACAGCGTTTCTGGACCTCCACCTCAGACTCA 3245
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3001 GAGCCCCTGCCTCTGAGCGACACCCTGCTCTGAGCCCGAGAGCTGTGAGCGCCGTGAGCCAGC 3060
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Db  3246 GAGCCCCTGCCTCTGAGCGACACCCTGCTCTGAGCCCGAGAGCTGTGAGCGCCGTGAGCCAGC 3305
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3061 TCTGAGGAAGGGGCTAGGACTGGGCGTCAGGGGCTCAGGGCCTTGCCCTGGGACCCCACCAGC 3120
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3306 TCTGAGGAAGGGGCTAGGACTGGGCGTCAGGGGCTCAGGGCCTTGCCCTGGGACCCCACCAGC 3365
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3121 ACTGGAGAGCCCCACCAGGGTCAGCTTATTGGCTGCCATGGCTCTGGCCACAGTCGACCAGAAGAAGGC 3180
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3366 ACTGGAGAGCCCCACCAGGGTCAGCTTATTGGCTGCCATGGCTCTGGCCACAGTCGACCAGAAGAAGGC 3425
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3181 GAGATGTGCTTATTGGCTGCCATGGCTCTGGCCACAGTCGACCAGTCGCCACAGTGGCACAGTCGACCAGTCGCC 3240
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3426 GAGATGGTGCTTATTGGCTGCCATGGCTCTGGCCACAGTCGACCAGTCGCCACAGTGGCACAGTCGACCAGGAGGC 3485
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3241 ACAGGGGTCTGA 3252
                ||||||||||||
Db  3486 ACAGGGGTCTGA 3497
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RESULT 7
AR281263
LOCUS         AR281263                  3355 bp    DNA      linear    PAT 10-APR-2003
DEFINITION    Sequence 1 from patent US 6518398.
ACCESSION     AR281263
VERSION       AR281263.1  GI:29716863
KEYWORDS      .
SOURCE        Unknown.
  ORGANISM    Unknown.
              Unclassified.
REFERENCE     1  (bases 1 to 3355)
  AUTHORS     Curtis,R.A.J.
  TITLE       ERG potassium channel.
  JOURNAL     Patent: US 6518398-A 1 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1..3355
                     /organism="unknown"
BASE COUNT      580 a    1128 c    1041 g     606 t
ORIGIN

Query Match             97.08%;  Score 3156;  DB 6;  Length 3355;
Best Local Similarity   98.28%;  Pred. No. 0;
Matches 3192;  Mismatches   0;  Conservative   0;  Indels   60;  Gaps   0;

Qy     1 ATGCCGGCCATGCGGGGCCTCCTCGGGCCTCAGAACACTTCCTGGACAACACTTCGTGCTACG 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   104 ATGCCGGCCATGCGGGGCCTCCTCGGGCCTCAGAACACTTCCTGGACAACACTTCGTGCTACG 163
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61 CGCTTCGACGGCCACGCACGTAACTTCGTTGCTGCTGGGCAACGCCCACGCCAGTGGCGGGCTCTTC 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   164 CGCTTCGACGGCCACGCACGTAACTTCGTTGCTGCTGGGCAACGCCCACGCCAGTGGCGGGCTCTTC 223
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 CCGGTGGTCTACTGCCTTCGTGACTCACGGGTTCTCGGGCTTCTCCGGGCTGAGGTC 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1866 TACTTCCAGGCCACCTGGGCCGTGAACAATGGCATCGACACCACCGAGCTGCTGCAGAGC 1925
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1681 CTCCCTGACGAGCTGCGCGCGGCCAGCGGCCATGCCAGCCACCTGCACAAGGAGGTCTGCAGCTG 1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1926 CTCCCTGACGAGCTGCGCGCGGCCAGCGGCCATGCCAGCCACCTGCACAAGGAGGTCCGCAGCTG 1965
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1741 CCACTGTTTGAGGCGGCCAGCCGGGCACTGTCTCTGCCGCCCGCCGGGCACTGGTCTCTGGCCCTCGGGGCCC 1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1986 CCACTGTTTGAGGCGGCCAGCCGGGCACTGTCTCTGCCGCCCGCCGGGCACTGGTCTCTGGCCCTCGGGGCCC 2045
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1801 GCCTTCTGCACGCCGGGCGAGTACTCATCACCAAGGCGATGCCCTGCAGGCCCTCAC 1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2046 GCCTTCTGCACGCCGGGCGAGTACTTCATCACCAAGGCGATGCCCTGCAGGCCCTCAC 2105
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1861 TTTGTCTGCTCTGCCTCCATGGAGGTGCTCAAGGGTCGCCATCCTAGGG 1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2106 TTTGTCTGCTCTGCCTCCATGGAGGTGCTCAAGGGTCGCCATCCTAGGG 2165
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1921 AAGGGCGACCTGATCGGCTGTGAGCTGCCCGGGGAGCAGTGTAAAGGCCAATCGC 1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2166 AAGGGCGACCTGATCGGCTGTGAGCTGCCCGGGGAGCAGTGTAAAGGCCAATCGC 2225
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1981 GACGTGAAGGGCTGACGTACTCGCTTCGGCTGTGTCTGCAGCTGGCTGGCTGGCTGCGACAC 2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2226 GACGTGAAGGGCTGACGTACTCGCTTCGGCTGTGTCTGCAGCTGGCTGGCTGGCTGCGACAC 2285
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2041 AGCCTTGCGCTGTACCCCGAGTTTGCCCGCGGCTTCAGTCGTGGCCTTCGAGGGGAGCTC 2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2286 AGCCTTGCGCTGTACCCCGAGTTTGCCCGCGGCTTCAGTCGTGGCCTTCGAGGGGAGCTC 2345
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2101 AGTACAAACCTGGGTGCTGGGGAGGCTCTGCGAGAGTGGACCAGCTGCCTGAGCCGGC 2160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2346 AGCTACAAACCTGGGTGCTGGGGAGGCTCTGCGAGAGTGGACCAGCTGCCTGAGCCGGC 2405
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2161 GACAATACCCTTATGTCCACGCTGGAGGAAGGAGACAGATGGGACAGGAGGGCCCACG 2220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2406 GACAATACCCTTATGTCCACGCTGGAGGAAGGAGACAGATGGGACAGGAGGGCCCACG 2465
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2221 GTCTCCCCAGCCAGCTGATGAGCCCTCCAGCCCCTGCTCCCCTGGCTGCACCTCC 2280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2466 GTCTCCCCAGCCAGCTGATGAGCCCTCCAGCCCCTGCTCCCCTGGCTGCACCTCC 2525
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2281 TCATCCTCAGCTGCCAAGCTGCCAAGCTGCTATCCCAGCTCCGAACAGCACCCCGGCCTCGTCTAGGT 2340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2526 TCATCCTCAGCTGCCAAGCTGCCAAGCTGCTATCCCAGCTCCGAACAGCACCCCGGCCTCGTCGTCTAGT 2585
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2341 GGCAGAGGGAGGCCAGCCAGGCAGGGCTGGCCCTCTGCTCCC 2400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2586 GGCAGAGGGAGGCCAGCCAGGCAGGGCTGGCCCTCTGCTCCC 2645
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2401 CCACGGCCCTAGAGGGCTACGGCTGCCCCATGCACGGAATGTGCCCCAGATCTG 2460
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2646 CCACGGCCCCTAGAGGGCTACGGCTGCCCCATGCACGGAATGTGCCCCAGATCTG 2705
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2461 AGCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTGGCTGGCACCAGCCCAAGTTCCT 2520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2706 AGCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTGGCTGGCACCAGCCCAAGTTCCT 2765
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2521 TTTCCGGTGGCCAGTCTGGCCGGAATGTAACGAGCCCCCTGGACCAGGAGAGC 2580
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2766 TTTCCGGTGGCCAGTCTGGCCGGAATGTAACGAGCCCCCTGGACCAGGAGAGC 2825
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2581 GGCCTGCTCACTGTTCCCCATGGGCCGGCAAGGACCAAGGAACACAGACACTTCCTGGACAACACTTCCTGGACAAG 2640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2826 GGCCTGCTCACTGTTCCCCATGGGCCGGCAAGGACCAAGGAACACAGACACTTCCTGGACAAG 2885
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2641 CTTCGGCGGCTGACAGAGCTGCTGGGGGAAGGACTGCGAG 2700
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2886 CTTCGGCGGCTGACAGAGCTGCTGGGGGAAGGACTGCGAG 2945
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2701 TCACTTCGCCAGGCTGTGCAGCTTGTCCTGCGGCGCCCCACAGGAGGGTCCGTGCCCTCGGAGGTC 2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   224  CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC   283
Qy   181  ATGCAGCGGGGCTGTGCCTGCCTCCTTTATGGGCCAGACACCAGTGAGCTGTCCGC     240
Db   284  ATGCAGCGGGGCTGTGCCTGCCTCCTTTATGGGCCAGACACCAGTGAGCTGTCCGC     343
Qy   241  CAACAGATCCGACGAGCCCTGGACGAGGAGTTCAAGGCTGAGCTGATCCTGTAC       300
Db   344  CAACAGATCCGACGAGCCCTGGACGAGGAGTTCAAGGCTGAGCTGATCCTGTAC       403
Qy   301  CGGAAGAGCGGGGCCTCCGTTCTCGGTGTCTCCTGGATGTGATACCATAAAGAA:GAGAAA  360
Db   404  CGGAAGAGCGGGGCTCCGTTCTCGGTGTCTCCTGGATGTGATACCATAAAGAATGAGAAA  463
Qy   361  GGGGAGGTGCGTCTCTCACAAGGACATCAGCGAAAACCAAGAACCGAGGG            420
Db   464  GGGGAGGTGCGTCTCTCACAAGGACATCAGTGAAACCAAGAACCGAGGG             523
Qy   421  GGCCCGACAGATGGAAGGAGACAGGTGGTGGCCGCGGATATGGCGGGCACGATCC        480
Db   524  GGCCCTGACAGATGGAAGGAGACAGCAGGTAGTGGCCGCGGATATGGCGCACCAATCC    583
Qy   481  AAAGGCTTCAATGCCAACCGCGGCCCGGAGCCCGGCCCGTGCTCTTACCACCTGTCCGGCAC  540
Db   584  AAAGGCTTCAATGCCAACCGCGGCCCGGAGCCCGGCCCGTGCTCTTACCACCTGTCCGGCAC  643
Qy   541  CTGCAGAAGCAGCAGCCCAAGGGCAAGCACACAGGTGTTGGGGAGAAACCA          600
Db   644  CTACTTCCAGGCCACCTGGCCGGGTCAATAAGGGGGTGTTTGGGGAGAAGCCA         703
Qy   601  AACTTGCCTGAGTACAAAGTAGCCGGCCGGCCCGTGCTCTTCATCCGTTGCACTGT      660
Db   704  AACTTGCCTGAGTACAAAGTAGCTGCCGGGCCCGTGCTCTTCATCCGTTGCACTGT      763
Qy   661  GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGTCTCCGCCCACACTCTATGTGGCTGTC  720
Db   764  GGGGCACTGAGGGGCCACCTGGGATGGCTTCATCCCGTCTCCGCCCACGTGCTGTC      823
Qy   721  ACTGTGCCCTACACAGGGTGTGTGTGAGCACAGACGCGGAGCCCAGTGCGCGCCGGGCCCG    780
Db   824  ACCGTGCCCTACAGCGGTGTGTGTGAGCACAGCACCGCGGAGCCCAGTGCGCGCCGGGCCCCA 883
Qy   781  CCCAGCGTCTGTGACCTGGCCCGGAGTCCTCTTCATCCTTGACATTGTCTGAATTTC       840
Db   884  CCCAGCGTCTGTGACCTGGCCGGGTCCTCTTCATCCTTCATCGTGCTGAATTTC          943
Qy   841  CGTACCACATCGTGTCCGTCCCAGTGGGTGTTGGGCCAGCGCGTCATCGGAGTCGTCGAATTCGCCTG 900
Db   944  CGTACCACATCGTGTCCGTCCCAGTGGGTGTTTGGGCCAGCGCGTCATCGGAGTCGCCATTGCCTC   1003
Qy   901  CACTACGTGCACCACCCACGTTCCTGCTGGA:GTCATCGGAGGCGCGGGCCCTTTGACCTGCC:A 960
Db   1004 CACTACGTCACCACCCACGTTCCTGCTGGATGTCATCGGAGGCGCTGGGCCCTTTGACCTGTC   1063
Qy   961  CATGCCTTCAAGGTCAACGTGTACCTGCTGCTGAAGACGTGCGCCCGCTG           1020
Db   1064 CATGCCTTCAAGGTCAACGTGTACCTGCTGCTGAAGACGTGCGCCCGCTG           1123
Qy   1021 CGGCTGCTGCCCTGCCTGGGCTCTCCGGGCTGGACACGGTACACGCGCCCGTGTGCTG       1080
Db   1124 CGGCTGCTGCCCTGCCTGGGCTCTCCGGGCTGGACACGGTACACGCGCCCGTGTGCTG       1183
Qy   1081 ACACTGCTCATGGGGCGGGAGATCGAGAGCACTGGCTCGCCGTGTTCGCCCTGTTCGCGGTCTGTTTAC  1140
Db   1184 ACACTGCTCATGGGGCGGGAGATCGAGAGCACTGGCTCGCCGTGTTCGCCCTGTTCGCGGTCTGTTTAC  1243
Qy   1141 ATTGGCCACCGGGGCCCTCCCTACTTGGTCGCTGGAGATTGGCTGGCTGCTGCAG        1200
Db   1244 ATTGGTCAGCGGGGGATCGAGAGCAGCGAGAATCCGAGCTGCTGGAGATTGGCTGGCTGCTGCAG       1303
Qy   1201 GAGCTGGCCCGCCGCCGGACTCCCTACTTGGTGGGCCGGAGGCCAGCTGGAGGG          1260
Db   1304 GAGCTGGCCCGCCGCCGGACCCCTACTTGGTGGGCCGGAGGACCAGCCGGAGGG          1363
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Db   1261 AACAGCTCCGGCACGAGTGACAACTGCAGCAGCGCAGCAGCCAGGCCAACGGGGACGGGGCTG       1320
Qy                                                                              
Db   1364 AACAGCTCTGGCCAGAGTGACAACTGCAGCAGCGCAGCAGCCAGGCCAACGGGGACGGGGCTG       1423
Qy   1321 GAGCTGCTGGGCGGCCGTGCTCGGCTGCGGGCCTACATCAGCCCCTCACTTCGCACTC           1380
Db   1424 GAGCTGCTAGGCGGCCGCCGTCGGCTGCGGGCCTACATCAGCCCCTCACTTCGCACTC           1483
Qy   1381 AGCAGCGCCTCACCAGCTGGGCTTCGGCAACGTGTCCCAACACGGACACCGAGAGATC            1440
Db   1484 AGCAGCGCCTCACCAGCTGGGCTTCGGCAACGTGTCCCAAC:ACGGACACTGAGAGATC            1543
Qy   1441 TTCTCCATCTGCACACATGCTCATCGGCGCCGCCATGGCCGGTGCACGGCGTGGTTTGGGAACGTG     1500
Db   1544 TTCTCCATCTGCACACATGCTCATCGGCGCCGCCATGGCCGGTGCACGGCGTGGTGTTCGGGAACGTG     1603
Qy   1501 ACGGCCATCATCCAGCGCCATGTGTACGCCGCGCTTTCTGTACCACCGCGCGGGCGAC            1560
Db   1604 ACGGCCATCATCCAGCGCCATGTGTACGCCGCGCTTTCTGTACCACCAGCGCCACCGGCGAC            1663
Qy   1561 CTGCGCGACTACATCGCATCCCGATCACCACCACCTCCCAAGCGCCCTAAGCAGCAGCATGCTGGAG   1620
Db   1664 CTGCGCGACTACATCCGATCACCACCTATCCCAAGCGCCCTAAGCAGCAGCATGCTGGAG           1723
Qy   1621 TACTTCCAGGCCACCTGGGCGGTGAACAATGCATCGCATCGACAACATCGCGCACTGCTGCAGAGC    1680
Db   1724 TACTTCCAGGCCACCTGGGCGGTGAACAATGCATCGCATCGACAACATCGCGCACTGCTGCAGAGC    1783
Qy   1681 CTCCCTGACGAGCTGCGGCCGCAGAGATCGCGCACCTGCGCGACAAGGAGGTCCTGCAGGTG        1740
Db   1784 CTCCCTGACGAGCTGCGGCCGCAGAGATCGCGCACCTGCGCGACAAGGAGGTCCTGCAGGTG        1843
Qy   1741 CCACTGTTTGAGGCGGCGCCAGCGCACTGCTCTCTGCGGGCCC                            1800
Db   1844 CCGGTGTTTGAGGCGGCGCCAGCGCACTGCTCTCTGCGGGCCC                            1903
Qy   1801 GCCTTCTGCACGCCGGGAGTACCTCATCCACCAGGCCGATGCCCTGCAGGCCCTCTAC            1860
Db   1904 GCCTTCTGCACGCCGGGAGTACCTCATCCACCAGGCCGATGCCCTGCAGGCCCTCTAC            1963
Qy   1861 TTTGTCTGCTGCTGGGCTCATGGAGGTGCTCCATGGTGCACCGTGCTCGTCTCCATCCTAGGG       1920
Db   1964 TTTGTCTGCTCCTGTGGCTCCATGGAGGTGCTCCATGGTGCACCGTGCTCGTCTCCATCCTAGGG       2023
Qy   1921 AAGGGCGACCTGATCGGCTTGTGAGCGTGGCGGGCGCAGTGGTAAAGGCCAATGCC              1980
Db   2024 AAGGTGACCTGATCGGCTGTGAGCGTGGCGGGCGCAGTGGTAAAGGCCAACGCC                2083
Qy   1981 GACGTGAAGGGCTGACGTACTGCTGGCCTGCAGTGTCTGCAGTGTCTGCCTGCACGAC             2040
Db   2084 GATGTGAAGGGCGTGACGTACTGCTGGCCTGCAGTGTCTGCAGTGTCTGCCTGCACGAC             2143
Qy   2041 AGCCTTGCGCTGTACCCCGAGTTGCCCCGACGTTGCGCGCCTGCTC                        2100
Db   2144 AGCCTTGCGCTCACCCCGACGTTGCCCCGACGTGCCCGGGAGCTC                         2203
Qy   2101 AGTACAACCTGGGCTGCTGGGGAGGCTCTGCAGAGGTGGACACCAGCTCCCTGAGCGGC           2160
Db   2204 AGTACAACCTGGGCTGCTGGGGAGGCTCTGCAGAGGTGGACACCAGCTCCCTGAGCGGC           2263
Qy   2161 GACAATACCCTTATGTCCAGCTGATGAGCCCTCAGAGCCCTGCTGGCCCACG                  2220
Db   2264 GACAATACCCTTATGTCCAGCTGATGAGCCCCAGAGCCCCACACCCCCACCA                  2323
Qy   2221 GTCTCCCAGCTGCCAAGTCTGCTATCCCCACCTGCGTGTCCCCTGGCTGCTGCAGGAGCTC          2280
Db   2324 GTCTCCCAGCTGCCAAGTCTGCTATCCCCACTGTCCCCTGGTTGCACCTCC                   2383
Qy   2281 TCATCCTCCGGCTGCCAAGCTGCTATCCCCGAACAGCACCCGGCCTCGTCTAGGT               2340
Db   2384 TCATCCTCCGGCTGCCAAGCTGCTATCCCCGAACAGCACCCGGCCTCGTCTAGGT               2443
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Qy   2341  GGCAGAGGGAGGCCAGGCAGGGCTTTGAAGGCTGAGGCTGCCCCTGCTCCC  2400
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2444  GGCAGAGGGAGGACCAGGCAGGGCTTTGAAGGCTGAGGCTGCCCCTGCTCCC  2503

Qy   2401  CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCATGGAATGTGCCCAGATCTG  2460
                |||||||||||||||||| .....|||||||||||||||||||||||||||
Db   2504  CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCATGCATGGAATGTGCCCAGATCTG  2563

Qy   2461  AGCCCAGGGTAGTAGATGGCATTGAAGACGGCTCGGACCAGCCAAGTTCTCT  2520
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2564  AGCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACCAGCCAAGTTCTCT  2623

Qy   2521  TTCCGGTGGCCAGTCTGGCCCGGAATGTAGCAGGAGAGCCCCTCCCCTGGACCAGAGAGAGC  2580
                ||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   2624  TTCCGGTGGCCAGTC·GGCCGGAATGTAGCAGCAGGGCCCCTCCCCTGGACCAGAGAGT  2683

Qy   2581  GGCCTGCTCACTGTCCCCTACTGTCTGCAGCCGCCCCCAATGGGCAACACTTCCTGGACCACCA·CGCTACG  2640
                ||||||||||||||||||||||||||||||||||||||||||||| .....|||| ||| |||
Db   2684  GGCCTGCTCACTG·CCCCTACTGTCCCCTACTGTCTGCAGCCGCCCCCAATGGGCAACACTTCCTGGACCACCATCCGCTACG  2743

Qy   2641  CTTCGGCAGGGGGTGACAGAGTCTGTCAGATGCGGGAAGGACTGCAG·CGCTCTTC  2700
                ||||||||||||||||||| |||||||| | |||||||||||||||
Db   2744  CTTCGGCAGGGGTGATGGAGCTGTGCAGATGCGGGAAGGACTGCAG  2803

Qy   2701  TCACTTCGCCAGGCTGTGCAGCTTGTCCTGGGGCCCCACAGGGAGGGTCCGTGCCCCTGGG  2760
                |||||||||||||||||||||||||| | |||||||||||||||||||
Db   2804  TCACTTCGCCAGGCTGTGCAGCTTGTCCTGCTG·GCACCCCATAGGGAGGGTCATGCCCCTGGG  2863

Qy   2761  GCATCGGGACGGGGGGCCGTGCCCGTGCCGCCAGCCAGCACCTCCGGGGCTTCTGCAGCCTCTCTGTGTG  2820
                ||| ||||||||||||||| ||||||||||||||||||||||||||||||| |
Db   2864  GCCTCAGGAGAGGGGCCGTGCCCATGCCGCCAGCCAGCACCTCCGGGGCTTCTGCAGCCTCTCTGTGTG  2923

Qy   2821  GACACTGGGGCATCCTCCTACTGTCCTCGCAGCCCCCACTGGCTGCTGTCTGAGTGGGACT  2880
                ||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   2924  GACACTGGGGCATCC·ACTGCCTCGCAGCCCCCACTGGCTCTGTGTCTGAGTGGGACT  2983

Qy   2881  TGGGCCCACCCTCGTCCTCGGGGGCCATCCCCTCATGCCGCACCCTGCCCTGGGGTCCCCCA  2940
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2984  TGGGCCCCACCCTCGTCCTCGGGGGCCATCCCCTCATGCCGCACCCTGCCCTGGGGTCCCCCA  3043

Qy   2941  GCGTCTCAGGTCTCCCCCTGCTCGAGCAGC·TTCTGGACCTCCACCTCCAGACTCA  3000
                ||||||||||||||||||||||||||||||  |||||||||||||||||||||
Db   3044  GCATCTCAGCTCTCCCCCTGCTCGAGCAGCCAGCTTCTGCACCTCCACCTCCAGACTCA  3103

Qy   3001  GAGCCCCTGCCTCAGGAGGACCCTCGTCTGAGGCCTGCGCCCAGCACCCCCTCCCCTCCTCCI  3060
                |||||||||||||||||||||||||||| |||||||||||||||||||| |||
Db   3104  GAGCCCCCTGCCTCGCTCGCTGAGGCCTGCGCCCAGCACCCCCTCCCCTCACCTCCTCCT  3163

Qy   3061  TCTGAGGAAGGGGCTAGGGACTCGGGCCCGCAGAGCCTGTGAGCCGAGGCTGAGGCTACCAGC  3120
                ||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   3164  TCTGAGGAAGGGGCTAGGGACTGGGCCCCAGAGCCTGTGAGCCGAGGCTGAGGCTACCAGC  3223

Qy   3121  ACTGGAGAGCCCCCCGCCGCCAGGGTCAGGGGCCTCGGCCTCAGGGGACCCCACAGCCTG  3180
                ||||||||||||||||||||||||||||||||||||||||||||||
Db   3224  ACTGGAGAGCAGCCCCCGCCGTCCAGTGCCCTGCCCTGGGGGTCCCCACAGCCTG  3283

Qy   3181  GAGATGTGCTATTGCTGCCCATGGCTCTCGGCACAGTACAAAGTACCGCCATCCGGAAGAAGGC  3240
                |||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   3284  GAGATGTGCTATTGGCTGCCACGGCTCTCGGCACAGTACAAAGTACCGCCATCCGGAAGAAGGC  3343

Qy   3241  ACAGGGGTCTGA  3252
                ||||||||||||
Db   3344  ACAGGGGTCTGA  3355
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Qy   1    ATGCCGGCCATGCGGGGCCTCGCGCCTCAGGAACACCTTCCTGGACCACCA·CGCTACG  60
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Db   1    ATGCCGGCCATGCGGGGCCTCGCGCCTCGGCGCCGCAGAACACCTTCCTGGACCACCTCCTACG  60
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(continued alignment blocks on right column — see above)

RESULT 8

AR281264

LOCUS   AR281264   3249 bp   DNA   linear   PAT 10-APR-2003

DEFINITION Sequence 3 from patent US 6518398.

ACCESSION   AR281264

VERSION   AR281264.1 GI:29716864

KEYWORDS   .

SOURCE   Unknown.

  ORGANISM Unknown.
            Unclassified.

REFERENCE   1 (bases 1 to 3249)

  AUTHORS   Curtis,R.A.J.

  TITLE   ERG potassium channel

  JOURNAL   Patent: US 6518398-A 3 11-FEB-2003;

FEATURES   Location/Qualifiers

     source   1..3249
                     /organism="unknown"

BASE COUNT   570 a   1089 c   990 g   600 t

ORIGIN

Query Match   97.0%; Score 3153; DB 6; Length 3249;
Best Local Similarity   98.2%; Pred. No. 0;
Matches 3189; Conservative   0; Mismatches   60; Indels   0; Gaps   0;

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Qy  1980 AAGGGTGACCTGATCGGCCTGTGTGAGCTGCCCGGAGGGAGCAGGTGTAAAGGCCAACGCC 1980
Db   901 CACTACGTCACCACCTGGTTCCTGCTGGATGTCATGCAGCGCTGCCCTTTGACCTGCTA   960
Qy  2040 GACGTGAAGGGGCTGACGTACTGCGTCCTGCTGGTGCTGCTGGCTGGCTGCCTGCACGAC 2040
Db   901 CACTACGTCACCACCTGGTTCCTGCTGGATGTCATGCAGCGCTGCCCTTTGACCTGCTA   960

Qy  2040 GATCTGAAGGGGCTGACGTACTGCGTCCTGCTGGTGCTGCTGGCTGGCTGCCTGCACGAC 2040
Db   961 CATGCCTTCAAGGTCACGGTTACTTCGGGCCCATCTGCTGAAGACGTGCGCGTGCTGCTG 1020

Qy  2100 AGCCTTGGCGTGTACCCCGAGTTGCCCGCGCTTCAGTGTGGCCTCCGAGGGGAGCTC 2100
Db   961 CATGCCTTCAAGGTCACGGTTACTTCGGGCCCATCTGCTGAAGACGTGCGCGTGCTGCTG 1020

Qy  2100 AGCCTTGGCGTGTACCCCGAGTTGCCCGCGCTTCAGCCGCTGGCCTCCGAGGGGAGCTC 2100
Db  1020 CGGCCTGCGTCGCGCTGCTTCCGCCGCTGGACCGGGTACTACGCCGCCTGGTGTGCTG 1080

Qy  2150 AGCTACAACCTGGGTGCTGGGGGAGGCGCTTGCAGACGTGGACACCAGCTCCCTGAGCGGC 2150
Db  1020 CGGCCTGCGTCGCGCTGCTTCCGCCGCTGGACCGGGTACTACAGCGCCGCCTGGTGTGCTG 1080

Qy  2160 AGCTACAACCTGGGTGCTGGGGGAGGCGCTTGCAGACGTGGACACCAGCTCCCTGAGCGGC 2160
Db  1080 ACACTGCTCATGGGCCGTGTTCGGCCACTGGCTCCGCCACTGGCTCCGCTCTGCTGGTT-TAC 1140

Qy  2220 GACAATACCCTTATGTCCACGCGGGAGGAGAAGGAGAGACAATGGGGAGCAGGGGCCCACG 2220
Db  1080 ACACTGCTCATGGGCCGTGTTCGGCCACTGGCTCCGCCACTGGCTCCGCTCTGGTTGTTTAC 1140

Qy  2220 GACAATACCCTTATGTCCACGCGGGAGGAGAAGGAGAGACAGATGGGAGGCAGGGCCCCACA 2220
Db  1140 ATTGGCCAGCGGGAGATCGAGACGCAGCGAATCCAGCTCCTGAGATTGGCCTGGCTGCAG 1200

Qy  2280 GTCTCCCCAGCCCCAGCTCGATGAGCCCTGCTGGGGGGAGGCTTGCAGACGTGGACACCTCC 2280
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Qy  2280 GTCTCCCCAGCCCCAGCTGATGAGCCCTGCTGGGGGGAGGCTTGCAGACGTGGACACCTCC 2280
Db  1200 GAGCTGGCCGCCGCGACTGAGTCCATGGGCCGACTGGGCGTCGGTGTGGGTCTGTGGAGGG 1260

Qy  2340 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGCACCCCGGCTCGTCGTCTAGGT 2340
Db  1200 GAGCTGGTCGCGCCGACTGAGTCCATGGGCCGACTGGGCGTCGGTGTGGGTCTGTGGAGGG 1260

Qy  2340 TCATCCTCGGCTGCCAAGCTGCTATCCCCACGTCGAACAGCACCCCGGCTCGTCGTCTAGGT 2340
Db  1260 AACAGCTTCCGGCCAGAGTGACAACTGCAGCAGCAGCGAGGCCAACTGCAGGGACGGGGCTG 1320

Qy  2400 GGCAGAGGAGGGCCAGGGAGGGCAGGGCAGGGCAGGGCTGGCCCTCTCGCTCCC 2400
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Qy  2400 GGCAGAGGAGGGCCAGGGAGGGCAGGGCAGGGCAGGGCTTGAAGGCTGAAGGCTGGCCCTCTCGCTCCC 2400
Db  1320 ACACAGCTCTGGCCAGAGTGACACTGCAGCGCTTACACCTTCCCTCTTCGCACTC 1380

Qy  2460 CCACGCGGGCCTAGAGGGGTACGGGCTGCCCCCATGGGAATGGACTCGCTTACTGCACTCTG 2460
Db  1320 ACACAGCTCTGGCCAGAGTGACACTGCAGCGCTTACACCTTCCCTCTTCGCACTC 1380

Qy  2460 CCACGCGGGCCTAGAGGGGTACGGGCTGCCCCCATGGGAATGGACTCGCTTACTGCACTC 2460
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Qy  2520 AGCCCCAGGGTAGTAGATGGCATTGAAGACGGCGTGTGGCTCGGACCAGCCCAAGTTCTCT 2520
Db  1380 AGCAGCCTCACCAGCGTGGGCTTCGGCCAACGTGTCCGCAACACGGACACCGGGAGAGATC 1440

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Db  1440 TTCTCCATCTGCACCATGCCATCGGGCGGCCTGATGCACGCGGTGGTGTTTGGGAACGTG 1500

Qy  2580 TTCCGCTGGTGGGCCAGTCGTTCCCCATGGGCCAGGGCCAGGGACACACTGGACACAG 2580
Db  1440 TTCTCCATCTGCACCATGCCATCGGGCGGCCTGATGCACGCGGTGGTGTTTGGGAACGTG 1500

Qy  2580 TTCCGCATGGGGCCAGTCGTTCCCCATGGGCCAGGGCCAGGGACACCACTGGACACAG 2580
Db  1500 ACGGGCCATCATCAGCAGCGCCATGTACGCCCGCGCCGTTTCTGTACCACAGCGGCCACGGCCGAC 1560

Qy  2640 GGCCTGCTCAC-GTTCCCCATGGGCCAGCGGCCACGCCCGGACCGGGCACAGGACACTGGACAGAG 2640
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Qy  2640 GGCCTGCTCACTGTCACTGTCCCCATGGGCCAGCGGCCACGCCCGGACCAGCAGCACCACTGGACAAAG 2640
Db  1560 CTGCGCAGGACTACCGGCATCCGGCATCCGCAIGCCCATCGCTGCACAAGGCCATCGTGTGCTGGAT 1620

Qy  2700 CTTCGGCAGGCGGGTGACAGAGCTGTCAGAGGACCAGTGCTGCTCAGAGGAGGTCCGTGCAG 2700
Db  1560 CTGCGCGACTACCGGCATCCGGCATCCGCAIGCCCATCGCTGCACAAGGCCATCGTGTGCTGGAT 1620

Qy  2700 CTTCGGCAGGCGGTGATGGAGCTGTCAGAGGACCAGTGCTGCTCAGAGGAGGACTACAG 2700
Db  1620 TACTTCCAGGGCGGTGAACAATGGCATGGACACCAAGGCGATGCCTGCTCGCAGACC 1680

Qy  2760 TCACTTCGGCCAGGCGTGTGCCAGTTGTCCTGGCACCACCTGGCACCCTCGG 2760
Db  1620 TACTTCCAGGGCGGTGAACAATGGCATGGACACCAAGGCGATGCCTGCTCGCAGAGC 1680

Qy  2760 TCACTTCGGCCAGGCGTGTGCCAGTTGTCCTGGCACCACCTGGCATGCCCCTCGG 2760
Db  1680 CTGCGCGACTACCGGCTATCCCCAGCCCTCAAGCTGCACAAGGACACGTGCTCCAGCTG 1740

Qy  2820 GCATCGGGAGAGGGGCCCGACAGAGCTGTCAGAGCCAGGTGCTCAGCCCCCATAGGGAGGACTGCAG 2820
Db  1680 CTGCGCGACTACCGGCTATCCCCAGCCCTCAAGCTGCACAAGGACACGTGCTCCAGCTG 1740

Qy  2820 GCCTCAGGAGGGGCCCGACAGAGCTGTCAGAGCCAGGTGCTCAGCCCCCATAGGGAGGACTCAG 2820
Db  1740 CCACTGTTGAGGCGGCAGCCGCCGCGCGGTGCTCTCGCTGCGCCTGCCCTGGCGGCCC 1800

Qy  2880 GACACTGGGCATCTCTACTCCTGCCCGGCTCCTCCGTCCGGGCTCCGGCCTGGGGGTCCCCA 2880
Db  1740 CCGGCTGTTTGAGGCGGCAGCCGCATCCGCGCGGTGCTCTCGCTGCGCCTGCCCTGGCGGCCC 1800

Qy  2880 GACACTGGGCATCTCTACTCCTGCCCGGCTCCTCCGTCCGGGCTCCGGCCTGGGGGTCCCCA 2880
Db  1800 GCCTTCTGCACGCGGGAGTACGTCTCATCGACAAGGCAGGTGCTTGCAGGCCCTCTAC 1860

Qy  2940 TGGCCCCACCCTCGTCCGGGCCTCCTCCCCTACGGCCACGCTTCTGAGCCTCACCTCAGACTCA 2940
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Qy  2940 TGGCCCCACCCTCGTCCGGGCCTCCTCCCCTACGGCCACGCTTCTGAGCCTCACCTCTAC 2940
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Qy  3000 GCGTCTCAGAGCTCCCCCGGCCTCCGGCCTGCCTCGCCATCCTAGGGGCC 3000
Db  1860 TTGTCTGCTCTGGCTCTCGATGGAGGTGCTCAAGGTGCTGGCACCGTGCTTCCGCAGCTG 1920

Qy  3000 GCATCTCAGAGCTCCCCCGGCCTCCGGCCTGCCTCGCCATCCTAGGGGCC 3000
Db  1920 AAGGGCCAGACCTGCATCGGCTGCGTGAGCTGCTGCGGGGGAGCAGGTGGTAAAGGCCAATGCC 1980

Qy  3060 GAGCCCCTGCCTCGCTGCCTCTGGAGGACCTGCTTCTGCGGAGACCTGAGCCCCGTCCTCCT 3060
Db  1920 AAGGGCCAGACCTGCATCGGCTGCGTGAGCTGCTGCGGGGGAGCAGGTGGTAAAGGCCAATGCC 1980

Qy  3060 GAGCCCCTGCCTCGCTGCCTCTGGAGGACCTGCTTCTGCGGAGACCTGAGCCCCGTCCTCCT 3060
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Qy    3061  TCTGGAGAACGGGGCTAGGACTGGGCCCAGGAGCCTGTGAGCCAGGCTACCAGC  3120
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Db    3061 "CTTGGAGAAGGGGCTAGGACTGGGCCCCACCAGCCTGTGAGCCAGGCTACCAGC  3120

Qy    3121  ACTGGAGAGAGCCCCACCAGGTCAGGGGGGCTGGCCTTGCCCTGGACCCCACAGCCTG  3180
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Db    3121  ACTGGAGAGCCCCCAGTCAGGGGGGCCTGGCCTTGCCCTGGGACCCCACAGCCTG  3189

Qy    3181  GAGATGGTGCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCAGGAAGAAGGC  3240
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Db    3181  GAGATGGTGCTTATTGGCTGCTGCCACGCTCTGCACAGTCCAGTGGACCAGGAAGAAGGC  3240

Db    3241  ACAGGGGTC  3249
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Db    3241  ACAGGGGTC  3249


BASE COUNT    738 a    1113 c    1034 g    710 t
ORIGIN

Qy Match
Best Local Similarity  81.9%;  Score 2654.8;  DB 10;  Length 3595;
                       89.0%;  Pred. No. 0;
Matches 2905;  Conservative  0;  Mismatches 347;  Indels 12;  Gaps  2;

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Qy    61  CGCTTCGACGGCACGGCACGCACAGTAACTTCTGGCCACGCCCAGGTGGCGGGGCTCTTC  120
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Db    81  CGCTTCGACGGCACGGCACGCACAGTAACTTCTGTCCTGGCCACGCCCAGGTGGCAGGGCTCTTC  140

Qy   121  CCCGTGGTCTACTGCTCGATGGCTTCTGTGACCAAGGAGTTCTCCCGGGCTGAGGTC  180
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Qy   181  ATGCAGCGGGCTGTGCCTCGTCCTCTTATGGGCCAGACACCAGTAGCTCGTCCGC  240
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Qy   241  CAACAGATCCGCAAGGCCCTGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC  300
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Qy   301  CGGAAGAGCGGGCTCCGTTCTGGTGCCTCCTGATGTGATAACCCATAAAGAAGAAGAGAAA  360
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Db   321  CGGAAGAGCGGGCTTCCATTCTGGTTCCTGGATGTGATACCCTTGGAGATGACCTATAAAAAACCAGAAG  380

Qy   361  GGGGAGGTGGCTCTTCTCCAGTCTTCTCCACAAGGACATCAGCGAAGCCAAGAACCGAGAGG  420
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Qy   421  GGCCCCGACAGATGGAAGGACCAGGTGGTGCCCAGGCCGGCCGATATGGCGGGGCACGATCC  480
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Db   441  GGCCCCGACAGATGGAAGGAGGAGGTGGTGCCCAGGCCGCCGATATGGCTCGGGCAGGATCC  480

Qy   481  AAAGGCTTCAATGCCAACCGGCGCCGGCCGGTCTCTCTACCACCTGTCTCGGGCAC  540
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Qy   541  CTGCAGAGAAGCAGCCACAAGGGCAAGCACAGCTCAATAGGGGGTGTTGGGGAAAACCA  600
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Qy   601  AACTTGCCTGAGTACAAAGTAGCGCCATCCGGAAGTCGCCCTTCA CCTGTTGCACTGT  660
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Db   621  AATTTGCCCGAATATAAAGTCGCTGCTATCCGATCGCTGGAAGTCACCCTTTATCCTGCTGCACTGT  680

Qy   661  GGGGCACTGAGAGCCACCGTGGCTGGATGGCTTCATCCTGCGCCACACTCTATGTGGCTGTC  720
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Db   681  GGGGCCTGAGAAGTGGGCCGTGGGATGGCTTCATCCTGCGCCACCTACGTGGCGTGTC  740

Qy   721  ACTGTGCCCTAGACGGTGTGTGAGCACGACGCACGGAGCCCAGCCGTGCCGCCGGCCCCCC  780
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Db   741  ACTGTGCCCATACAGCGTGTGTGAGCACGACGCACGGAGCCCAGTGCTCCCCGGTGCCCA  800

Qy   781  CCCAGGCTCTGACCCTCGGCTGGCCGTGGAGTCCTTCATCCTTGCTGAATTTC  840
          |||  | |||| ||| |||| |  ||||||||| ||||| |||||||||| |||
Db   801  CCTAGTGTCTGGACCTGGCCGTGGAAGTCCTTCA CTTAGTATTGTGCTGAATTTT  860

Qy   841  CGTACCACCATTCGTGTCCTGACGTGGGCCCAGTGGTGTTGCCCCAAAGTCATTGCCTC  900
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Db   861  CGTACTACTTGTGTCCAAGTGGTGATTCCCAAGTGGTGATTGCCCCAAAGTCATTGCCTC  920

Qy   901  CACTACGTCACCCACCTGTTCCTGCTGAATGTCATCGCAGCGTCGCTGCCCTTGACCTGCTA  960
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RESULT 9
RNO7627
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DEFINITION Rattus norvegicus mRNA for ELK channel 2.
ACCESSION   AJ007627
VERSION   AJ007627.1 GI:3702613
KEYWORDS   elk2 gene; potassium channel.
SOURCE   Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
AUTHORS   Engeland,B., Neu,A., Ludwig,J., Kooper,J. and Pongs,O.
TITLE   Identification of three rat potassium channel genes homologous to
            D. melanogaster elk
JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 3595)
AUTHORS   Engeland,B.
TITLE   Direct Submission
JOURNAL   Submitted (03-JUL-1998) Engeland B., Zentrum fuer Molekulare
            Neurobiologie Hamburg, Institut fuer Neurale Signalverarbeitung,
            Martinistrasse, D-20246 Hamburg, GERMANY
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                     KGFANRRSRAVLYHLSGHLGKQPKGKHKLNKGYVFGEKPNLPEYKVAAIFKSPFILL
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                     LPEIGWLQELARRLETPYYLVSRSPDGGNSSGQSENCSSSGGSEANGTGLELLGGPS
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                     VCSGSMEVLKGGTVLAILGKDLIGCELPEROQVVKANADVRGLTYCVLQCLQLAGLH
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                     GPSAHPRTLDGLQLPMPWNVPPDLSPRVVGIEDGGSGDQHKFSFRVGQSGGPECSSS"

Db   921 CACTACGGTCACCACCTGGTTCTTGCTGGAGTCATAGCAGCACTGCCCTTTGACCTACTA 980

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Qy   2032 CTGCACGACAGCCGCTGGGCTGTACCCGGAGTTTGTCCCGGCTTCAGTCGTCGTGGCCTCCGA 2091
           |||||| ||| |||| |||||  |||  ||  ||  ||||| ||| | |||| |||||||||||
Db   2061 CTGCACGAGGAGCGCTTCGCCACTGTACCCTGAGTTTGCCCCACCGCTTTAGCCGTTGGCCTCCGA 2120

Qy   2092 GGGGAGCTCAGCTACAACCTGGTGTCCGGGGAGGCTTCTGCAGAGGTGGACACCAGCTCC 2151
           |||||||||||  ||||  ||||||| | ||||||||  || ||||| |||||||||||
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Qy   2152 CTGAGCGGCGACAATACCCTTATGTCCACCCTGGAGGAGGAGACAGATGCGGAGCAG 2211
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Db   2181 CTGAGTGGTGACACACCCCTCATGTCCACCCTGGAGGAGGACGATGGGGACCAA 2240

Qy   2212 GGCCCACGGTCTCCCCACGGCCCCAGCTGATGAGCCCTCCAGCCCTGCCTGCCTGGC 2271
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Db   2241 GGACACACGGTCTCCAGCAGTCCCAGCAGATGAGCCCTCCAGCCCTGCCTGTCACCTGGC 2300

Qy   2272 TGCACCTCCCATCCAGCTGCCAAGTCTGCTATCCCCACGTGCAACAGCACCCCGGCCT 2331
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Db   2301 TGTACCTCCTCTCCTCCCTCCAGCGGCCAAACTACTCTCCCCACGTCGAACTGCACCCCGGCCG 2350

Qy   2332 CGTCTAGGTGGCAGAGGGAGGCCCTAGAGGGGCCTACGGCTGCCCCATGGAATGTGCCC 2391
           |  |  ||||| || ||||||| |||| ||||||  |||| |||||| ||| |||||
Db   2361 AGGGTGGGTGGCAGAGGGGCGGCCAAGTAGGGCAGGGGTTTGAAGCTGGCTGGTCCT 2420

Qy   2392 TCTGCTCCCCCACGGGCCCTAGAGGGCTACGGCTGCCCCTAC 2451
           |||||  || |||||||||| ||  | |||||| || |||
Db   2421 TCTGCTCATCCAGCGACACTTGATGGTTGCAGCTGTCGGCCTGACCT 2480

Qy   2452 CCAGATCTGAGCCCCAGGGTAGTAGATGGGCCAGTCGTGTGGCTCGACCAGCCC 2511
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Qy   2512 AAGTTCTCTTTCCGCGTGCTGGCCCAGTCTGTCCAGTGTGTCCCCCTGGA 2572
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Db   2541 AAGTTCTCTTTCCGGGTGCTGGCCCAGTCTGTCCAGCTCATCCTGGTGCCCCAAGGGAAGGCCAGGA 2600

Qy   2572 CCAGAGAGCGGCGCTGCTCACTGTTCCCATGGCCCAGCAAGGCAAGGGCAACACAGACACA 2631
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Db   2601 ACAGAGAGTGGCGCTGCTCACTGTCGCCGTGTGCCCAGTGAGCCAGTGAAGCAGAAACACAGACACA 2660

Qy   2632 CTGGACAAGCTCGGCAGGGTGACAGAGCTGTCAGACGAGCAGATGCGGGAA 2691
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Db   2661 CTGGACAAGCTACGGCAGGCGTGACGGAGCTGTCTGAACAGTGCTGCAGATGCCAGAG 2720

Qy   2692 GGACTGCAGTCACTCGCCAGGCTGTGCAGTTGTCCTGGCCCCACAGGGAGGGGTCCG 2751
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Qy   2812 CTGTGTGGACACTGGGGCATCCCTACTGCTGCCCCCGCCGCTGCTGTCTGTCTG 2871
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Db   2841 CTGCGTGTGGACACTGGGGCATCATCCTACTGCCTCTACTGCTGCGCAGGTTCAGTCGTTG 2900

Qy   2872 AGTGGGACTTGCCCCCACCCTCGTCCGGGGCCT--CCTCCCCTCATGGCACCTGGCCC 2928
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Db   2901 AGTGGGACTTGCCCTCCTCCCTCGTCCGCCATCCCCTGGCTTCATGCACCTGGCCC 2960

Qy   2929 TGGGGTCCCCCAGGCGTCTCAGAGCTCCCCCAGCCCCACCACAGCTTTCTGGACCTCC 2988
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Qy   2989 ACCTCAGACTTGCCCCCAGAGGCGTCTGCCCCTGGCCTCTGAGCCCAGCACCCCGCC 3048
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Qy   3049 TCCCCTCCTTCTGAGGAAGGGCTAGGACTGGGCCCCGCAGAGCCTGTGAGCTGGCTGGC 3108
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Db   3081 TCACCCCCTCCTTCTGAGGAAGGGACTAGGACTGGGGACTGTCCCAGTGCCTCCAGTCTGGGTGG 3140
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Qy   3109 GAGGCTACCAGCACTGGAGAGCCCCACCAGGGTCAGGGGGCCTGGCCTGCCCTGGGAC 3168
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RESULT 10
AR179195
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DEFINITION  Sequence 9 from patent US 6326168.
ACCESSION   AR79195
VERSION     AR79195.1  GI:20220750
KEYWORDS
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 3715)
  AUTHORS   Miyake,A., Mochizuki,S. and Yokoi,H.
  TITLE     Brain specific potassium channel protein
  JOURNAL   Patent: US 6326168-A 9 04-DEC-2001;
FEATURES    Location/Qualifiers
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BASE COUNT  735 a  1167 c  1090 g   723 t
ORIGIN

Query Match    81.9%;  Score 2664.8;  DB 6;  Length 3715;
Best Local Similarity   89.0%;  Pred. No. 0;
Matches 2905;  Conservative   0;  Mismatches  347;  Indels   12;  Gaps    2;

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Qy    181 ATGCAGCGGGGCTGTGCCTGGCCTGCCTGGCCGGCCGGGGCCCACACCAGTGAGCTCGTCCGC 240
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Db    396 CAACAGATCCCGGAAAAGCCCTGGATGAGCACAAGCAAAGAATTCAAGGCTGAGCTCTGTAC 455

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(Second column — alignment continuation)

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Qy    601 AACTTGCTGAGTACAAAGTAGCCGCCATCGGAAGTCGCCCTTCATCGTCGTTGCACTGT 660
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Qy    901 CACTACGTCACCACCTGGTTCCTGCTGCTGTGTCATCAGCACGCTGCCCTTTGACCTGCTA 960
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Qy   1612 ATCGTGGAGTACTTCCAGGCACTGGGGGTGAACAATGCATCGGGCGGTGAACACCACCGGCTG 1671
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The page consists of two columns of nucleotide sequence alignment blocks (labelled Db and Qy) with flanking position numbers, followed by a GenBank-format record.

Left column (position numbers, Db/Qy labels):
1776, 1672, 1836, 1732, 1896, 1792, 1956, 1852, 2016, 1912, 2076, 1972, 2136, 2032, 2196, 2092, 2256, 2152, 2316, 2212, 2376, 2272, 2436, 2332, 2496, 2392, 2556, 2452, 2616, 2512, 2676, 2572, 2736, 2632, 2796, 2692

Right column (position numbers, Db/Qy labels):
2856, 2752, 2916, 2812, 2976, 2872, 3036, 2929, 3096, 2969, 3156, 3049, 3216, 3109, 3276, 3169, 3336, 3229, 3396

Ending positions: 1835, 1791, 1895, 1791, 1955, 1851, 2015, 1911, 2075, 1971, 2135, 2031, 2195, 2091, 2255, 2151, 2315, 2211, 2375, 2271, 2435, 2331, 2495, 2391, 2555, 2451, 2615, 2511, 2675, 2571, 2735, 2631, 2795, 2691, 2855, 2751

Right column ending positions: 2915, 2811, 2975, 2871, 3035, 2928, 3095, 2988, 3155, 3048, 3215, 3108, 3275, 3168, 3335, 3228, 3395, 3252, 3419

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ORIGIN
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Db  1056  CACTACGTCACCACCTGGTTCTCCTGGATGTCATAGCAGCACTGCCTTGACCTACTA   1115

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Qy   3109 GAGGCTACCAGCACTGGAGAGCCCCACCAGGGTCAGGGGTCAGGGGCCGTGGGAC 3168
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Db   3276 GAGGCTACCAGTACTGGAGAGCCCCCTCCGGGTCAGGGGCCGAGCCTTGCCCTGGGAT 3335
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Qy   3169 CCCCACAGCCTGGAGATGTGCTTATTGGCGTGCCATGGCTCTGGCACAGTCCAGTGGACC 3228
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Db   3336 CCCCACAGCCTAGAGATGGTGTCATCGGCTGCCATGGCCTGGCTCGGTCTCCACTGGACC 3395
               |||||||||||||||||||||
Qy   3229 CAGGAAGAAGGCACAGGGGTCTGA 3252
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Db   3396 CAGGAGGAGGGCACAGGAGTCTGA 3419
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RESULT 12
AF109143

LOCUS       AF109143          3615 bp    mRNA            linear   ROD 24-JUN-1999
DEFINITION  Mus musculus ether-a-go-go-like potassium channel (Elk2) mRNA,
            complete cds.
ACCESSION   AF109143
VERSION     AF109143.1  GI:5163194
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
REFERENCE   1  (bases 1 to 3615)
  AUTHORS   Trudeau,M.C., Titus,S.A., Branchaw,J.L., Ganetzky,B. and
            Robertson,G.A.
  TITLE     Functional analysis of a mouse brain Elk-type K+ channel
  JOURNAL   J. Neurosci. 19 (8), 2906-2918 (1999)
  MEDLINE   99208772
   PUBMED   10191308
REFERENCE   2  (bases 1 to 3615)
  AUTHORS   Titus,S.A., Ganetzky,B.S., Robertson,G.A., Trudeau,M.C. and
            Branchaw,J.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-NOV-1998) Genetics, UW-Madison, 445 Henry Mall,
            Madison, WI 53703, USA
FEATURES             Location/Qualifiers
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Db   1896 CTGCAGCTGCCATTGTTCGAGGCAGCGAGCCGTGCCTGGGGCACTGTCTTCGGGCC 1955
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Db   2016 GCTCTCTACTTTGTGTGCTCAGTTCCATGGAGGTCCTCATGGAGGTCCTCTCGCC 2075
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Qy   1912 ATCCTAGGGAAGGGCGACCTGATCGGCTGTGACTGGCCCGCCTGTGACCTGGTAAAG 1971
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Db   2076 ATTCTAGGGAAGGGTGACCTGATCGGCTGTGACTGGCCCGCCTGTGACCTGGTAAG TAGTGAAG 2135
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Qy   1972 GCCAATGCCGACGTGACTGGTGAGGGGCTGACTGCTCCTCAGTGTCTGCTGGCC 2031
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Db   2136 GCCAATGCCGACGTAAAGGGCTGACTGCTCCTACAGTGCCTGCAGCTGGCTGGG 2195
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Qy   2032 CTGCACGACAGCCTTGGCTGTACCCCGAGTTTGCCCGCGCTTCAGTCGTGCTCCGA 2091
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Qy   2152 CTGAGCCGGCGACAATACCCTTATGTCACGCTGATGAGCCTGTCCCCTGGC 2211
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Db   2316 CTGAGTCGTGACAACACCCTCATGTCCACACTGGAGGAGTGGGGAGCAA 2375
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Qy   2212 GGCCCCACGGTCTCCCCAGCCCAGCTGATGAGCCCTGCGTCCCCTGGC 2271
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Db   2376 GGACACACGATCTCACCAGCCCCAGAGTGAGCCCTGCGTGCACTGGC 2435
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Qy   2272 TGCACCCCTCATCCTCCAGCTGCCAAGCTCTATCCCCACGTGGAACACACCCCCGGCCT 2331
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Db   2436 TGTACCTCCTCGTCCTCAGCGGCCAAACTACTCTCCCCACGTGGAACTGAACTGGAATGTACCC 2495
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Qy   2332 CGTCTAGGTGGCAGAGGGAGGAGGCGCCAGGCAGGCAGGCTTGAAGGCTGAGGCTGCCCC 2391
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Db   2496 AGGCTGGGTGGCAGAGGGCGGGCCAAGTAGGGCGAGGCAGGGTTTGAAGCCTGAGGCTGGTGCCC 2555
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Qy   2392 TCTGCTCCCCCACGGGCCCTAGAGGGGCTACGGCGTGCCCCCATGCCATGGAATGTGCCC 2451
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Qy   2452 CCAGATCTGAGCCCCCAGGGTAGTAGATGGCATTGAAGACGCGTGTGGGCTCGGACCAGCCC 2511
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Qy   2752 TGCCCTCGGGATCGGACACTGGGCAGGAGGGGCATCCTCCTGCTACTGCCCTGCCCTGCTCTTG 2811
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ORIGIN

Query Match     81.8%;  Score  2660.8;  DB 10;  Length 3615;
Best Local Similarity   88.9%;
Matches  2901;  Mismatches   349;  Indels  12;  Gaps  2;
Conservative  2;  Pred. No. 0:
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Qy  3109 GAGGCTACCAGCACTGGAGAGCCCCCACCAGGTCAGGGGCCTGGCCTTCCCCTGGGAC 3168
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Qy  3169 CCCCACCAGCCTGGAGATGGTGCTTATTGGCTCCATGGCTGCCATGGCCAGTCCAGTGGACC 3228
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Db  3204 CCCCACCAGCCTAGAGATGGTGCTCATCGGGTGCTGCCATGCCCTGGCTCGTCGTCCAGTGGACC 3263

Qy  3229 CAGGAAGAGGCACAGGGGTCTGA 3252
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RESULT 13
BC033141

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LOCUS       BC033141                1432 bp    mRNA    linear   PRI 27-JUN-2002
DEFINITION  Homo sapiens, clone IMAGE:3944793, mRNA, partial cds.
ACCESSION   BC033141
VERSION     BC033141.1  GI:21620039
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1432)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapps-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
            Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
            Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
            Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
            Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
            Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
            Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
            George Yang, Scott Zuyderduyn, Marco Marra.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 43 Row: C Column: 13
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Qy  1912 ATCCTAGGGAAGGGCCGACCTGATCGGCTGTGAGCTGCCCGGCGGGAGCAGGTGTAAAG 1971
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Db  1944 ATTCTAGGGAAGGGTGACCTGACTGGCTGTACGGCGTGACCGAGAGCAAGTAGTGAAG 2003

Qy  1972 GCCAATGCCGACGTGAACGGGCTGACCTACTGCTCTGCTCAGTGTCTGCAGTGGCTGGC 2031
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Qy  2032 CTGCACGACAGCCTTGCGCCTGTACCCCGAGTTGCCCCGCGTTCAGTCGTGGCCTCCGA 2091
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Db  2064 CTGCACGAGAGCCTCGCACTGTACCCCACGCGCTTTGCCCGGCGTGGCGTGGCCTCCGA 2123

Qy  2092 GGGAGCTCAGCTACAACCTGGTGCTGGGGAGGCTGCAGASGTGGACACCAGGTCC 2151
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Db  2124 GGGAGCTCAGCTACAACCTGGGTGGAGAGTGTCTGCAGAGTGCTGCAGGTGGACTCA 2183

Qy  2152 CTGAGCGGCGACAATACCCTTATGTCACGCTGGAGGAAGGAGACAGAGATGGGGAGCAG 2211
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Db  2184 CTGAGTGGTGACAACACCCTTCATGTCCACACTGGAGGAAGGAGAGAGATGGGGAGCAA 2243

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Qy  2272 TGCACCTCCTCATCCTCAGCTGCCAAGCTGCTATCCCCACCGTCGCAACAGCACCCCGGCCT 2331
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Db  2304 TGTACCTCCTCCTCCCTCAGCGGCCAAACTACTCTCCCCACGCTGCACCCCCGGCCGCCCGCG 2363

Qy  2332 CGTCTAGGTGGCAGAGGGAGGCAGGCAGGCAGGGTTTGAAGGCTGAGGCTGGCCCC 2391
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Qy  2392 TCTGCTCCCCCACGGGCGGCCTAGAGGGGCTACGGCTGCCCCCCATGCCATGGAATGTGCCC 2451
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Db  2424 TCTGCTCATCCACGGACACTTGATGGGGTTGCAGCTGCCTGCCCCCATGCCATGGAATGTACCT 2483

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Qy  2572 CCAGAGAGCCGGCCTGCTCACTGTTCCCCATGGCCCAGCGGCCCGAGGCAAGGAACACAGACACA 2631
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Qy  2632 CTGGACAAGCTTCGGCAGGCGGTGACAGAGCGTCAGGATGCGGAA 2691
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Qy  2812 CTGTGTGTGGACACTGGGCCATCCTCCTACTGCCCTGCAGCCCCCAGTCGGCTCTGTCTTG 2871
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ORIGIN

Query Match     32.58;     Score 1055.4;  DB 9;   Length 1432;
Best Local Similarity  99.9%;   Pred. No. 3.1e-159;
Matches 1056;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db     1  GACAGATGGGGAGCAGGCCCCCAGCCTCTCCCAGCCCTGATGAGCCCTCCAGCCC    60

Qy  2256  CCTGCTGTCCCCTGGCTGCACCTCCTCATCCTCAGCTGCCAAGCTGTATCCCCACGTCG  2315
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Qy  2316  AACAGCACCCCGGCCTCGTCTAGGTGGCAGAGGAGGCAGGCAGGGGCTTTGAA  2375
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Db   121  AACAGCACCCCGGCCTCGTCTAGGTGGCAGAGGAGGCAGGCAGGGGCTTTGAA   180

Qy  2376  GGCTGAGGCTGGCCCCTTGCTCCCCCAGCGGGCCTAGAGGGGCTGCCCCCAT  2435
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Qy  2436  GCCATGGAATGTGCCCCCAGAATCTGAGCCCCAGGTAGTAGATGGCATTGAAGACGGGTG  2495
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Qy  2496  TGGCTCGGACCAGCCCAAGTTCTCTTTCCGGCGTGGGCCAGTCTGGCCCGGAAGTAGCAG  2555
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Qy  2556  CAGCCCCTCCCCTGGACCAGAGAGCGGGGCTGCCCACTGTCCCCATGGGCCCAGCGAGGC  2615
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Db   361  CAGCCCCTCCCCTGGACCAGAGAGCGGGGCTGCCCACTGTCCCCATGGGCCCAGCGAGGC   420

Qy  2616  AAGGAACACAGACACTGGACAAGCTGTCGGTGACAGCGTGTCAGAGCCAGGT  2675
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  AAGGAACACAGACACTGGACAAGCTGTCGGTGACAGCGTGTCAGAGCCAGGT   480

Qy  2676  GCTGCAGATGCGGAAGGACTCACTTCGGCCAGTCACTTCCTGTCCTTGTCCTGGCGCC  2735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  GCTGCAGATGCGGAAGGACTCACTTCGGCCAGTCACTTCCTGTCCTTGTCCTGGCGCC   540

Qy  2736  CCACAGGGAGGGTCCGTGCCCTCGGGAGCGGCCATGCGGGGCCGTGCCCAGCCAGCACTC  2795
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Db   541  CCACAGGGAGGGTCCGTGCCCTCGGGAGCGGCCATGCGGGGCCGTGCCCAGCCAGCACTC   600

Qy  2796  CGGGCTTCAGCCTGTGTGGACTGGGCATCCTCTACTGCCTGCGCCCCTCAGCCCCC  2855
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  CGGGCTTCAGCCTGTGTGGACTGGGCATCCTCTACTGCCTGCGCCCCTCAGCCCCC   660

Qy  2856  AGCTGGCTCTGTCTGTTGAGTGGGACTTGGCCCCCACCCTGTCTCCTGCCCTCTCCCCAT  2915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  AGCTGGCTCTGTCTGTTGAGTGGGACTTGGCCCCCACCCTGTCTCCTGCCCTCTCCCCAT   720

Qy  2916  GGCACCCTGGCCCTGGGGTCCCCAGCGTCAGAGCTCAGCCTCCCTGGCCTGAGCCAGCAGC  2975
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Db   721  GGCACCCTGGCCC:GGGGTCCCCAGCGTCTCAGAGCTCCCCGGCCTGAGCC  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2976  TTTCTGACCTCCACCTCAGACTCAGAGCCCCTGCCTCAGGAGACCTCTGCTCTGAGCC  3035
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Db   781  TTTCTGACCTCCACCTCAGACTCAGAGCCCCTGCCTCAGGAGACCTCTGCTCTGAGCC  840

Qy  3036  CAGCACCCCTGCCTCCCTCCTCCTTCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCC  3095
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Db   841  CAGCACCCCTGCCTCCCTCCTCCTTCTGAGGAAGGGCTAGGACTGGGCCCGCAGAGCC  900

Qy  3096  TGTGAGCCAGGCTACCAGCACTGGAGAGCCCCCACCAGGGTCAGGGGCCTGGC  3155
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  TGTGAGCCAGGCTACCAGCACTGGAGAGCCCCCACCAGGGTCAGGGGCCTGGC  960

Qy  3156  CTTGCCCTGGGACCCCCACAGCCTGGGAGATGGTGCTTATTGGTGCCATGGCTCTCGGCAC  3215
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961  CTTGCCCTGGGACCCCCACAGCCTGGGAGATGGTGCTTATTGGTGCCATGGCTCTCGGCAC  1020

Qy  3216  AGTCCAGTGGACCCAGGAAGAGGAGGCACAGGGGTCTGA  3252
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RESULT 14
AR179192
LOCUS        AR179192                  3064 bp    DNA         linear   PAT 20-APR-2002
DEFINITION   Sequence 5 from patent US 6326168.
ACCESSION    AR179192
VERSION      AR179192.1   GI:20220747
KEYWORDS     .
SOURCE       Unknown.
  ORGANISM   Unknown.
             Unclassified.
REFERENCE    1  (bases 1 to 3064)
  AUTHORS    Miyake,A., Mochizuki,S. and Yokoi,H.
  TITLE      Brain specific potassium channel protein
  JOURNAL    Patent: US 6326168-A 5 04-DEC-2001;
FEATURES             Location/Qualifiers
  source          1..3064
                  /organism="unknown"
BASE COUNT     554 a     1042 c     848 g     620 t
ORIGIN

Query Match     27.2%;    Score 884.8;   DB 6;   Length 3064;
Best Local Similarity  65.5%;   Pred. No. 5.5e-132;
Matches 408;  Conservative  0;  Mismatches  622;  Indels  120;  Gaps  3;

Qy     1  ATGCCGGCCATGCGGGGCCTCCTCGGCGCCTCCAGGACACCTTCCTCGACACATCGGTACG    60
          ||||||||  ||||||   ||  ||  | |||||  |||||||  |||
Db     4  ATGCCGGTCATGAGGGGTTGCTCGGCCCCGGCAAAACACCTTCCTGACACCATCGCCACC    63

Qy    61  CCTTCGACGGCACGCACGACGTAACTTCGTCTGCTGGCAACGCCCAGTGGGGGGCTCTTC   120
          ||||||||  ||  |||  ||||  | |||||   || ||||  || ||||
Db    64  CGTTTGACGGACGAACGCACAGCAACTCTCGTCTGCTGGCAACGCCCAACGGGGCTTT   123

Qy   121  CCCGTGGTCTACTGCTCGATGGCTTCTCTGTCCTGGCGCTTGTCCCGGGCTGAGGTC   180
          ||| || || ||||  || | ||||| | || ||  |||| || ||  ||| |||
Db   124  CCCATCGTCTACTGCTCCGACGGCTTCTCGAGCTCTCGCGTCACACCGAGCTCACCGAGGTC   183

Qy   181  ATGCAGCGGGGCTGCGTCGCAGCTGGAGGGCCGTGCTGGAGAGGGCCAGCACCTG   240
          ||||| | |||||| ||   ||||||   || | |||| | ||||||  ||
Db   184  ATGCAGAAGACCCTGGACAAGCTGCGCCCGGTTTCCCTACGGCCCAGAGCAGTGAGCTCGTCCGC   243

Qy   241  CAACAGATCCGCAAGGCCCTGGACGCGGCATCTCCTACTGCCTGCGCTCGTGATCCGTAC   300
          ||||| |  ||  ||||  | || ||| ||  | || |||| || | ||  |||
Db   244  CAGCGTGCTGCACAAAGCCCTGGACGCGGCATCTCCTACTGCCTGCGCGGGTCTGAAATCTGCTCTAC   303

Qy   301  CGGAAGAGCGGCGGCTCCCCGGTTCCCGGTGTCTCCGGATGTGATAACACCATAAAGAAAGAATGAGAAA   360
          |||| || |  | ||  ||| | || | |||  || |  ||||  ||  || ||||||  | |||||
Db   304  CGCAAGGATGGCGGCTCAGCCTTTGGGTGCCTCTGGACGATGAGCCCATCAAGGACATGAGATG   363

Qy   361  GGGGAGGTGGCTCTTCTTCCTAGTCTCCAGCAGC------AGCAAACCAGAAC   414
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Db   364 GGGGAGGCCGTGCTGTTCCTCTTTTCCTTCAAGGTATCACTCAGAGTGGAAGCCCAGGA 423

Qy   415 CGAGGGGGCCCGACAGATGGAAGGAGACAGTGGTGGCCGGCCGCATATGGCCGGGCA 474
Db   424 CTTGGCCCCCAAGGAGGCCGCGGGGACAGTAATCACGAAAAACTCCCTGGGGTAGAAGGGGA 485

Qy   475 CGATCCAAAGGCTTCAATGCCAACCGGCGGGAGCCGGCCGTGCTGCTTACCACCTGTCC 534
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Qy   535 GGGCACCTGCAGAAGCAGCAGCAGCCCAAGGGCAAGGCTCAATAAAGGGGTGTTTGGGGAG 594
Db   544 GGCCACCTTTGGCGCCGGCCAGGGGAGGGCAATGGAAGGCCAATAATAAACGTGTTTGAGCCA 603

Qy   595 AAACCAAACTGCCTGAGTACAAAGTAGCCGCCATCCGGAGTCGCCTTCATCCTGTTG 654
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Qy   715 GCTGTCACTGCTGCCTACAGCGTGTGTGAGCACAGCAGCAGGGGTGTTTGGGCCGCCGC 774
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Qy   775 GGCCCGCCCAGGGTCTGTGACCTGGAGGTCCTCTCATCCTTGACATGTGCTG 834
Db   784 CGACACACCCTTGTCAGCGACATCGCCGTGAAATGCTCTTCATCCTAGATATCATCCTG 843

Qy   835 AATTTCCGTACCACATTCGTGTCCAAGTCGGGCGTCTTTGCCCAAAGTCCATT 894
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Qy   895 TGCCTCCACTACGTCACCACCTGGTTCCTCCTGCTGGTTCCTCGCAGCCGTTTGAC 954
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Qy   955 CTGCTACTAGCCTTCAAGGTCAACGTGACTTCGGGGCCATCTGAGAAGACGGTGCGC 1014
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Qy   1015 CTGCTGCGCCTGCTGCGCCTCCTTCCGGCTCACCGGGCTACTGCAGGTACAGCGCCGCG 1074
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Qy   1075 GTGCTGACACTGCTCATGGCCGGTGTTCCGCCGGTGTTCGCGGTCGCCTCCGTCTGG 1134
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Qy   1135 TTTTACATTGGCCAGCGGCGGAGATCGAGCAGCAGCGAATCCGAGCTGCCTGAGATTGGCGG 1194
Db   1144 TATGTCATCGGGGGCGGGGGACGATGAGGGCCAATGACCCGGCTGCTCGTTGGGACATTGGCTGG 1203

Qy   1195 CTGCAGGAGCTGGCCCCCGACTGGAGACTCCTACTACCGTGTGGGCCGGAGGCCAGCT 1254
Db   1204 TTGCCATGAGTTGGGCAAGCCTCTCGAGGTGCCCTATGTCAATGGCTC---------- 1250

Qy   1255 GGAGGGGAACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGGCCAGCGAGGCCAACGGGACG 1314
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Qy   1315 GGGCTGGAGCTGTGGGCCGCGGCCCTGCGCAGCGCCTACACCTCCCTCTTC 1374
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Qy   1375 GCACTCAGCAGCGCCTCACCAGCGTGGCCGCTTCGGCAACGCCTTCGCGCCAACATCACCGGGCCGGACACCGAG 1434
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Qy   1435 AAGATCTTCTCCATCTGCACCAGGATGCTCATGGCCGCTAGGCCCCTGGGTCGGGGTGGTTGGG 1494
Db   1360 AAGATCTTCTCCATCTGCACGATGCTCATGGCCGCTAGGCCCTGGGTCGGGGTGTTCGGG 1419

Db   1495 AACGTGACGGCCATCATCCAGCCATGTACGCGCCCCGGCTTCTGTACCACAGCAGCCCACG 1554

Qy   1420 AACGTGACAGCCATCATCCAGCCAGGCTGGCCGGCCGCGTGCCGGCCGCTCCTACCACACCGCCGCATG 1473

Db   1555 CCGACCTGCGCCACTACATCCGATCCACGTATCCCCAAGCCCCGTATCCCAGCAGCCGCGATG 1614

Qy   1480 AAGGACCTCAAGGACTTCATCGGTGCACCGGCCGCCCGGCGGCCGTCAAGCCACCACCGAGTGCATG 1539

Db   1615 CTGGAGTACTTCCAGGCCACCTGGGCGTGGAACAATGGGATCGACACCGCCACCGAGTGCTG 1674

Qy   1540 CTCGAAATCTTCCAGACCACCTGGGCCGTCAACACGCGCATCGACGCCAACGAGTTACTG 1599

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Qy   1600 CGTGACTTCCCAGCAGAGCTGAGAGCTGACATTGCTATGCACCTGAATCGGGAGATCCTG 1659

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Qy   1660 CAGCTGCGTTGTTCGGGGCAGGCGAGCGAGGCAGGGGCTGCCTGGGCCCTATCGCTGCACATC 1719

Db   1795 CGGCCCGCCTTCTGCACGCCCGGCGGGGCGGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCC 1854

Qy   1720 AAGAACCTTCGTTCTCGCGCC·CGGGGCAGTACCTGTTGCGCCGTGTGGCCTGCAGGCA 1779

Db   1855 CTCTACTTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGCTCAAGGTGCTGCTCGGCATC 1914

Qy   1780 CATTACTATGTCTGTCCGCCCCTGAGCATGTGGCTG 1839

Db   1915 CTAGGGAAGGGGACCTGAGTCGTGGAGCTGCCCGGCGGAGCAG--------- 1962

Qy   1840 CTGGGAAGGGGACCTGATTGGAGCAGATATCCCTGACCGGGCCAGGAGCCTGGGTTG 1899

Db   1963 -------------GTGGTAAAGGCCAATGCCACGTGAAGGGCTGACGGACTGC 2004

Qy   1900 GGAGCAGACCCAAACTTCGTGCTAAAGACCAGTGGTGCTGATGTGAAAGCTTCTGAACCTACTGT 1959

Db   2005 GTCCTGCAGTGTCTGCAGCCTGCTGGCCTGCTGGTCCCTGGTACCCCAGTTT 2064

Qy   1960 GGCCTGCAGCGTGAGCAGCCGAGGGCTGGCTGAGGTCTCATCCTGAGTAT 2019

Db   2065 GCCCCCGGCCTTCAGTCGTGGCCTCCGAGGGGAGCTCAGTCAGTGACTACAACCTGGG 2114

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RESULT 15

ABO22698

LOCUS　　　　ABO22698　　　　　　　　3920 bp　　　mRNA　　　　　linear　　PRI 31-AUG-1999

DEFINITION　Homo sapiens mRNA for BEC2, complete cds.

ACCESSION　　ABO22698

VERSION　　　ABO22698.1　　GI:5804787

KEYWORDS　　 BEC2; human BEC2.

SOURCE　　　 Homo sapiens (human)

ORGANISM　　 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE　　1 (sites)

AUTHORS　　　Miyake,A., Mochizuki,S., Yokoi,H., Kohda,M. and Furuichi,K.

TITLE　　　　New ether-a-go-go K(+) channel family members localized in human telencephalon

JOURNAL　　　J. Biol. Chem. 274 (35), 25018-25025 (1999)

MEDLINE　　　99386988

PUBMED　　　 10455180

REFERENCE　　2 (bases 1 to 3920)

AUTHORS　　　Miyake,A., Mochizuki,S., Yokoi,H., Kohda,M. and Furuichi,K.

TITLE　　　　Direct Submission

JOURNAL　　　Submitted (21-JAN-1999) Akira Miyake, Yamanouchi Pharmaceutical Co.,Ltd., Molecular Medicine Laboratories; 21 Miyukigaoka, Tsukuba, Ibaraki 305-8585, Japan (E-mail:miyake@yamanouchi.co.jp, Tel:81-298-52-5111(ex.3324), Fax:81-298-52-5444)

FEATURES　　　　　　　　　　　　　Location/Qualifiers

source　　　　　　　　　　　　1..3920

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BASE COUNT      696 a   1329 c   1120 g    775 t
ORIGIN

  Query Match             27.2%;  Score 884.8;  DB 9;  Length 3920;
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  Matches 1408;  Conservative    0;  Mismatches  622;  Indels  120;  Gaps    3;

Qy          1 ATGCCGGCCATGCGGGGCCTCCTGGCGCCTCAGAACACCTTCCTGGACACCATCGCTACG 60
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Qy         61 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGCCCAGGTGGCGGGGCTCTTC 120
              || || ||||| |||||||| |||||| |||||| |||||| ||||   |  ||  |||
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Qy        241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300
              || |   | | ||| ||||||||| |  ||| |||||  |  ||||||  |   | | |||
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Qy        301 CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA 360
              || |||   ||     | || ||||| ||||||||  |||| ||||| ||||||||||
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Db        694 GGGGAGGTCGTGCTGTTCCTCTTTTCCTTCAAGGATATCACTCAGAGTGGAAGCCCAGGA 753

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Qy        475 CGATCCAAAGGCTTCAATGCCAACCGGCGGCGGAGCCGGGCCGTGCTCTACCACCTGTCC 534
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Qy        595 AAACCAAACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTG 654
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Qy        715 GCTGTCACTGTGCCCTACAGCGTGTGTGTGAGCACAGCACGGGAGCCCAGTGCCGCCCGC 774
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Db       1054 GCGGTCACCGTCCCCTACAATGTCTGTTTCTCGGGTGACGATGACACCCCCATCACTTCG 1113

Qy        775 GGCCCGCCCAGCGTCTGTGACCTGGCCGTGGAGGTCCTCTTCATCCTTGACATTGTGCTG 834
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Db       1114 CGACACACCCTTGTCAGCGACATCGCCGTGGAAATGCTCTTCATCCTAGATATCATCCTG 1173

Qy        835 AATTTCCGTACCACATTCGTGTCCAAGTCGGGCCAGGTGGTGTTTGCCCCAAAGTCCATT 894
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               ||||||||||| |  ||||||||||| |  | ||  | || || || ||||||||||||
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Qy        955 CTGCTACATGCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCGC 1014
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Qy       1015 CTGCTGCGCCTGCTGCGCCTGCTTCCGCGGCTGGACCGGTACTCGCAGTACAGCGCCGTG 1074
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Db       1581 ------------------------------------------------------------ 1580

Qy       1315 GGGCTGGAGCTGCTGGGCGGCCCGTCGCTGCGCAGCGCCTACATCACCTCCCTCTACTTC 1374
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              |||||||| ||||||||||||||||||||| | |||||||  || ||||||||||||| |
Db       1750 AACGTGACAGCCATCATCCAGCGCATGTACTCGCGCCGCTCGCTCTACCACAGCCGCATG 1809

Qy       1555 CGCGACCTGCGCGACTACATCCGCATCCACCGTATCCCCAAGCCCCTCAAGCAGCGCATG 1614
                 |||||    |||| ||||||  | |||||  | ||   ||| |||||||||||||||
Db       1810 AAGGACCTCAAGGACTTCATCCGTGTGCACCGCCTGCCGCGGCCGCTCAAGCAGCGCATG 1869

Qy       1615 CTGGAGTACTTCCAGGCCACCTGGGCGGTGAACAATGGCATCGACACCACCGAGCTGCTG 1674
              || || |||||||||| |||| ||||| || ||||  ||||||||| ||| |||| | |||
Db       1870 CTCGAATACTTCCAGACCACGTGGGCCGTCAACAGCGGCATCGACGCCAACGAGTTACTG 1929
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`Thu Oct  2 09:06:43 2003`   us-09-965-830-1_copy_6_3257.rge

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Qy    1675  CAGAGCCTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCCTG  1734
                  | |||| |: ||||| :| ||||: | |||| || ||||:|| | ||: |||.:
Db    1930  CGTGACTTCCCAGACGAGCTGAGAGCTGACATTGC:ATGCACCTGAATCGGGAGATCCTG  1989

Qy    1735  CAGCTGCCACTGTTTGAGGCGGCCAGCCGGCTCCGGCCACTGTCTC:GGCCCTG  1794
                  ||||||||  |||| ; ||| :| ||| ' |||| |||||||| |: || |||  '
Db    1990  CAGCTGCCGTTGTTCGGGCACCGAGCCAGGGGCCTGCCTGCGGGCCCTATCGCTGCACATC  2049

Qy    1795  CGGCCCGCCTTCTGCACGCCGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCC  1854
                  | || | |||||| - :||||||:|||||  | | |  || |:|||||||:||||
Db    2050  AAGACCTCGTTCTGCGGCTCCGGCGAGTACCTGGCGGTTGCGCCGTGGGGATGCCCTGCAGGCA  2109

Qy    1855  CTCTACTTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGCTCGCCATC  1914
                  - |||| ||:|||||: ||||| -   || |||||||  |  || |-|||| | |'|||
Db    2110  CATTACTATGTCGCTCCCGGCTCCTTGAGCTGCTCCGAGACAACATGGTGCTGGCCATC  2169

Qy    1915  CTAGGGAAGGGCGACCTGATCGGCTGTGAGCTGCCCCGGCGGGACCAG---------  1962
                  ||  ||||| |  ||||| |||||| ||  | | |- |||  |||||  
Db    2170  CTGGGGAAGGGGACCTGATTGGAGCAGATATCCCTGAGCCGGGGCAGGAGCCTGGGTTG  2229

Qy    1963  --------GTGGTAAAGGCCAATGCCGACGTGAAGGGGCTGACGTACIGC  2004
                          :||||:|||| |:| ||||  ||||: |:||| :|||||:||:| |::: | |
Db    2230  GGAGCAGACGCCAAACTTCGTGCTTAAAGACCAGTGCTGAGTGAAAGCTCTGACCTACTGT  2289

Qy    2005  GTCCTGCAGTGTCTGCGAGC:GGCTGGCCTGCACGACAGCCTTGCCGCTGTACCCCGAGTTT  2064
                  | |||||||| ::|       || ||| :| ||| |:|| ||:|: :|||:
Db    2290  GCCTGCAGCAGCCTGAGCAGCCGAGGCTGGCTGGCTCCTGAGGCTCTATCCTGAGTAT  2349

Qy    2065  GCCCCGCCGCTTCAGTCGTGCCTTCCGAGGGGAGCTCAGTTACAACCTGGG  2114
                  | -| |:| | |||||| | |||||: | |||||||:|||:: |
Db    2350  GGGGCTGCCTTCCGGGGCTGGCCTTCCGGGGACCTCACCTTCAACCTGCG  2399
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Search completed: October 1, 2003, 19:33:24
Job time : 11469 secs

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                 GenCore version 5.1.6
         Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   October  1, 2003, 15:33:19 ; Search time 798 Seconds
                    (without alignments)
                    11000.717 Million cell updates/sec

Title:         US-09-965-830-1_COPY_6_3257
Perfect score: 3252
Sequence:    1 atgccgccatgcggggcct........aagaaggcacagggtctga 3252

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:    252756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters:      5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  N_Geneseq_19jun03:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	3252	100.0	3323	20	AAX84910	Human brain specif
2	3250.4	100.0	3829	21	AAZ87712	Human ESK1 (hESK1)
3	3245.8	99.8	3249	21	AAZ50119	Human Elk voltage
4	3244	99.8	3252	21	AAA14893	DNA encoding a her
5	3218	99.0	3857	22	AAZ11906	Human potassium ch
6	3156	97.0	3355	21	AAZ50452	Monkey potassium c
7	2664.8	81.9	3715	20	AAX84919	Rat brain specific
8	884.8	27.2	3064	20	AAX84911	Human brain specif
9	869.8	26.7	3736	20	AAX84918	Rat brain specific
10	844.4	26.0	1132	21	AA250454	Human potassium ch
11	794.4	24.4	3742	21	AA293334	Rat elk1 potassium
12	761.2	23.4	5107	21	AA250455	Human potassium ch
13	601	18.5	10579	22	ABA20014	Human nervous syst
14	601	18.5	10579	22	AAK70045	Human immune/haema
15	601	18.5	28995	22	ABA20015	Human nervous syst
16	601	18.5	28995	22	AAK70046	Human immune/haema
17	601	18.5	28995	22	AAK79967	Human immune/haema
18	601	18.5	28995	22	AAK85213	Human immune/haema
19	572.4	17.6	2694	21	AA250453	Human potassium ch:
20	561.2	17.3	20974	23	AAS92595	DNA encoding novel
21	384	11.8	464	21	AA293335	Rat elk2 potassium
22	355.6	11.2	3164	23	ABI08835	Human potassium ch
23	364.2	11.2	4112	23	ABX12009	Drosophila melanog
24	364	11.2	3135	25	ABK88234	Transporters and i
25	362.4	11.1	2746	24	AAL44675	Human erg2 (h-erg2
26	362.4	11.1	2877	24	ABK88231	Human transporter
27	362.4	11.1	2983	24	ABK88232	cDNA sequence enco
28	362.4	11.1	2983	24	ABK88233	cDNA sequence enco
29	362.4	11.1	3091	24	ABX12014	Human erg2 (h-erg2
30	347.2	10.7	2868	25	AAH21451	Transporters and i
31	342.8	10.5	3479	22	AAA07661	Human HERG1 DNA.
32	342.8	10.5	3480	21	AA235716	Long QT syndrome a
33	342.8	10.5	3950	21	AAA07602	Long QT syndrome a
34	342.8	10.5	4070	22	AAI66257	Human potassium ch
35	342.8	10.5	4070	22	AAF61965	Human eag-related
36	342.8	10.5	4070	25	ABZ76227	Human HERG potassi
37	333.6	10.4	1780	25	ABV75862	Human potassium ch
38	317.2	9.8	426	22	AAI98635	Human excretory re
39	317.2	9.8	426	22	AAI63031	Human kidney relat
40	303	9.3	2886	21	AA235716	Human potassium io
41	303	9.3	3002	21	AA235721	Human eag related
42	296	9.1	2746	25	ABX12013	Transporters and i
43	296	9.1	2779	24	AAD27279	Human transporter
44	290.8	8.9	350	22	ABA14086	Human nervous syst
45	281.2	8.6	2967	21	AA235717	Human potassium io

ALIGNMENTS

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RESULT 1
AAX84910
ID   AAX84910 standard; DNA; 3323 BP.
XX
AC   AAX84910;
XX
DT   28-SEP-1999  (first entry)
XX
DE   Human brain specific potassium channel protein coding sequence.
XX
KW   Brain specific potassium channel; human; central nervous system disorder;
KW   dementia; cerebral ischaemic sclerosis; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             6..3257
FT                   /*tag= a
XX
PN   WO9937577-A1.
XX
PD   29-JUL-1999.
XX
PF   20-JAN-1999; 99WO-JP00190.
XX
PR   04-DEC-1998; 98JP-0346198.
PR   23-JAN-1998; 98JP-0011434.
XX
PA   (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
PI   Miyake A, Mochizuki S, Yokoi H;
```

us-09-965-830-1_copy_6_3257.rng

```
XX
DR   WPI; 1999-458683/38.
DR   P-PSDB; AAY22426.
XX
PT   Potassium channel protein expressed specifically in brain tissue and
PT   method for its production
XX
PS   Claim 6; Page 33-39; 63pp; English.
XX
CC   This sequence encodes the potassium channel protein of the invention,
CC   that is expressed specifically in brain tissue. The protein is used to
CC   treat and investigate disorders of the central nervous system such as
CC   dementia and cerebral ischaemic sclerosis.
XX
SQ   Sequence 3323 BP; 577 A; 1121 C; 1018 G; 607 T; 0 other;

Query Match      100.0%;    Score 3252;    DB 20;    Length 3323;
Best Local Similarity   100.0%;
Matches 3252;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy      1 ATGCCGGCCATGCGGGGGCCTCCTGGCGCCTCAGAACACTTCCTGGACACCATCGCTACG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6 ATGCCGGCCATGCGGGGGCCTCCTGGCGCCTCAGAACACTTCCTGGACACCATCGCTACG 65

Qy     61 CGCTTCGACGGCACGCACGTAACTTCGTGCTGCTGGACCTCACGGGCTTCTCCCGGGCTGTTCTC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     66 CGCTTCGACGGCACGCACGTAACTTCGTGCTGCTGGACCTCACGGGCTTCTCCCGGGCTGTTCTC 125

Qy    121 CCCGTGGTCTACTGCTGCTGATGGTTCAAGGCACAACAGAGTTCAAGGCTGAGCTGATCCTGTAC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    181 ATGCAGCGGGGCTGTGCCTGCCTCCTTTATGGGCCAGTGAGCTCGCGCC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    186 ATGCAGCGGGGCTGTGCCTGCCTCCTTTATGGGCCAGTGAGCTCGCGCC 245

Qy    241 CAACAGATCCGCAAGCCCTGGACGAGCACAAGGACACAAGAGCCCTGGACGAGCACAAGGACA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    246 CAACAGATCCGCAAGCCCTGGACGAGCACAAGGACACAAGAGCCCTGGACGAGCACAAGGACA 305

Qy    301 CGGAAGAGCGGCGGCTCCCGTTCTCGGTGTCTCCTGGATGGATACCCATAAAGAATGAGAAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    361 GGGGGAGGTGGCTCTCTTCCAGTCTCCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420
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Qy    421 GGCCCGACGATGGAAGGAGACACAGGTGGTGCGGCGCGGGAGGCCGGGCGGCGGATATGGCCGGGACGATCC 480
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Qy    481 AAAGGCTTCAATCGCCAACGCCGCGGCCCGGGAGCCCGGGCTGCTCCAGCCCTGTCCGGGCAC 540
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Qy    541 CTGCAGAAGCAGCCCAAGGGCACAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600
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Qy    601 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCGTGTGCACTGT 660
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Qy    661 GGGGCACTGAGACGCGTGTGTGAGCACAGCACGCAGGACACCAGTGTCTCTGGC 720
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Qy    721 ACTGTCGCCTACAGCGTGTGTGAGCACAGCACGCAGGACACCAGTGTCTCTGGC 780
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Qy    841 CGTACCACATTCGTGTCCAAGTCGGCGCCAGGTGGTGTTGCCCAAAGTCCATTGCCTC 900
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Db    845 CGTACCACATTCGTGTCCAAGTCGGCGCCAGGTGGTGTTGCCCAAAGTCCATTGCCTC 905

Qy    901 CACTAGTCACCACCTGGTTCCTGCTGCGATGTCATCCGAGCGGCTGCCCTTGACCTGCTA 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    961 CATGCCGGCCCATCTGCTGAAGGTCAACGTACT-CGGGCGCCTGCCCTTGAAGACGG 1020
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Db    961 CATGCCGGCCCATCTGCTGAAGGTCAACGTACTTCGGGCGCCTGCCCTTGAAGACGG 1025

Qy   1021 CGCCTGCTGCGCCGCTTCCGGCGCCTGGACCGGTACTCGCAGTACAGGCCGTGGTGCTG 1080
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Qy   1081 ACACTGCTCATGCCGGTCGTTCGCCACTGGCTCGCCGAGTCGCTGCTGGTTTTAC 1140
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Qy   1141 ATTGGCCAGCGGGGAGATCGAGAGCAGCGAATCCGAGTCGCTGCTGAGATTGGCTGGCTGCAG 1200
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Qy   1201 GAGCTGCCCGACTGGAGCTCCCTACTACCTGGTGGGGCCGGAGGCCAGCTGGAGGG 1260
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Qy   1981 GACGTGAAGGGGCTGACGTACTGGCTGTCTGCAGTGTCTTGGCTGGCTGGACGCGACGAC 2040
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Qy   2161 GACAATACCCTTATGTCCAGCTGATGAGCCCTTCAGCCCCCTGCTGTCCCCTGCCACCTCC 2220
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Qy   2221 GTCTCCCCAGCCCCCAGCTGATGAGCCCTTCAGCCCCTCGTGTCCCCTGCTGCCACCTCC 2280
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Qy   2281 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGCACCCCGGCCTCGTCTAGGT 2340
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Qy   2401 CCACGGGCCCTAGAGGGGCTACGGCTGCCCCGCCATGGAATGTGCCCCAGATCTG 2460
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Qy   2461 AGCCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACCCCAAGTTCTCT 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   2466 AGCCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACCCCAAGTTCTCT 2525

Qy   2521 TTCGGCGTGGGGCCAGTCTGGCCCCGGAATGTAGCAGCAGCCCCTCCCCTGGACAGAGAGC 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   2526 TTCGGCGTGGGGCCAGTCTGGCCCCGGAATGTAGCAGCAGCCCCTCCCCTGGACAGAGAGC 2585

Qy   2581 GGCCGTGCTCACTGTTCCCCATGGCCCAGCGAGCCAAGGAACACAGAACACACTGACAAG 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2586 GGCCGTGCTCACTGTTCCCCATGGCCCAGCGAGCCAAGGAACACAGAACACACTGACAAG 2645

Qy   2641 CTTCGGCAGGAGAGGGGCGTGACAGAGCTGTCAGAGCAGTGCTGCGAGGATGCGGGAAGGACTGCAG 2700
          ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   2646 CTTCGGCAGGAGAGGGGCGTGACAGAGCTGTCAGAGCAGTGCTGCGAGGATGCGGGAAGGACTGCAG 2705

Qy   2701 TCACTTCCCAGGCTGTGCAGCTTGTCCTGGCCCCACAGGGAGGGTCCGTGCCCTCGG 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2706 TCACTTCCCAGGCTGTGCAGCTTGTCCTGGCCCCACAGGGAGGGTCCGTGCCCTCGG 2765

Qy   2761 GCATCGGGAGAGGGGCCGTGCCCAGCCAGCGCCCGTGCCCCAGGGCTTCTGCAGCCTCTGTGTGTG 2820
          |||||||||||||||||||||||||||||||| |||||||||||||||| |||||||||
Db   2766 GCATCGGGAGAGGGGCCGTGCCCAGCCAGCGCCCGTGCCCCAGGGCTTCTGCAGCCTCTGTGTGTG 2825

Qy   2821 GACACTGGGGCCATCCTCCTACTGCCTGAGCACTCCCAGCTGGCTCTTGAGTGGGACT 2880
          ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   2826 GACACTGGGGCATCCTCCTACTGCCTGAGCACTCCCAGCTGGCTCTTGAGTGGGACT 2885

Qy   2881 TGGCCCCACCCTGCTCCTCCCCATGGCACCCTGGGGTCCCCCA 2940
          ||||| |||| ||||||||| |||| ||| ||||| ||||||
Db   2886 TGGCCCCACCCTGCTCCTCCCCATGGCACCCTGGGGTCCCCCA 2945

Qy   2941 GGGTCTCAGAGCTCCCCCTGGCCTGGAGCCACCAGCTTCCGACCTCCACCTCAGACTCA 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2946 GCGTCTCAGAGCTCCCCCTGGCCTGGAGCCACCAGCTTTCTGGACCTCCACCTCAGACTCA 3005
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Db   3001 GAGCCCCTGCCTCGTCCAGGAGACCTCTGCTCTGAGCCCAGCACCCCTGCCTCCCCTCCTCCT 3060
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   3006 GAGCCCCCTGCCTCGTCCAGGAGACCTCTGCTCTGAGCCCAGCACCCCTGCCTCCCCTCCTCCT 3065

Qy   3061 TCTGAGGAAGGGGCTAGGACTGGCCCCGCAGAGCCTGTGAGCCTGAGGCTACCAGC 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3066 TCTGAGGAAGGGGCTAGGACTGGCCCCGCAGAGCCTGTGAGCCTGAGGCTACCAGC 3125

Qy   3121 ACTGGAGAGCCCCCACCAGGGTCAGGGGCTCAGGGGCCTGGCCTTGCCCTGGACCCCACACCCTG 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3126 ACTGGAGAGCCCCCACCAGGGTCAGGGGCCTCAGGGGCCTGGCCTTGCCCTGGACCCCACAGCCCTG 3185

Qy   3181 GAGATGGTGCTTATTGGCTGCCATGGCTCTCGGCACAGTCCAGTGACCCAGGAAGAAGGC 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3186 GAGATGGTGCTTATTGGCTGCCATGGCTCTCGGCACAGTCCAGTGACCCAGGAAGAAGGC 3245

Qy   3241 ACAGGGGTCTGA 3252
          ||||||||||||
Db   3246 ACAGGGGTCTGA 3257
```

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RESULT 2
AAZ87712
ID   AAZ87712 standard; DNA; 3829 BP.
XX
AC   AAZ87712;
XX
DT   19-MAY-2000  (first entry)
XX
DE   Human ESK1 (hESK1) protein encoding DNA.
XX
KW   ESK1; eag similar K+ channel; potassium channel associated disorder;
KW   neurological; Alzheimer's disease; anxiety; panic; autism; hyperactivity;
KW   obsessive-compulsive disorder; schizophrenia; Huntington's disease;
KW   epilepsy; cardiovascular; musculoskeletal; proliferative; cancer;
KW   ESK channel blocker; nootropic; neuroprotective; antidepressant;
KW   tranquilizer; neuroleptic; antiparkinsonian; cardiant; cytostatic;
KW   anticonvulsant; ds.
XX
OS   Homo sapiens.
XX
FH                Location/Qualifiers
FT   Key
FT   CDS           254..3496
FT                 /*tag= a
FT                 /product= "ESK1 protein"
XX
PN   WO200009534-A1.
XX
PD   24-FEB-2000.
XX
PF   13-AUG-1999;  99WO-US18556.
XX
PR   14-AUG-1998;  98US-0096570.
XX
PA   (ELAN-) ELAN PHARM INC.
XX
PI   Forsayeth JR, Zhao BB;
XX
DR   WPI; 2000-224270/19.
DR   P-PSDB; AAY77738.
XX
PT   Novel eag similar potassium channel polypeptide useful for treating
PT   various neurological, cardiovascular, musculoskeletal and proliferative
PT   disorders -
XX
PS   Claim 8; Fig 1A-F; 52pp; English.
XX
CC   This DNA encodes a eag similar K+ channel (ESK) polypeptide (hESK1). The
CC   hESK1 protein can be expressed by standard recombinant methodology. The
CC   ESK polypeptide, polynucleotides and antibodies are useful for treating
CC   and diagnosing various potassium channel associated disorders such as
CC   neurological disorders, e.g. Alzheimer's disease, depression, anxiety,
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CC   panic, obsessive-compulsive disorders, attention deficit, epilepsy,
CC   hyperactivity disorders, autism, schizophrenia, Huntington's disease and
CC   Parkinson's disease, cardiovascular disorders, musculoskeletal disorders
CC   and proliferative disorders such as cancer. The ESK polynucleotide is
CC   also useful for synthesis of FSK and gene mapping. The polypeptide can be
CC   used in an assay to identify molecules such as synthetic drugs,
CC   antibodies, peptides or other molecules which have an effect on the
CC   activity of the ESK channel.
XX
SQ   Sequence 3829 BP: 650 A: 1302 C: 1202 G: 675 T: 0 other;

Query Match   100.0%;   Score 3250.4; DB 21; Length 3829;
Best Local Similarity   100.0%; Pred. No. 0:
Matches 3251; Conservative 0: Mismatches 1; Indels 0; Gaps 0:

Qy   1 ATGCCGGCCATGGGGGCCTCCTGCGCGCCTTCCTGCGCGCCTTCCTGACACCATCGGCTACG   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   245 ATGCCGGCCATGGGGGCCTCCTGCGCGCCTTCCTGCGCGCCTTCCTGACACCATCGGCTACG 304

Qy   61 CGCTTCGACGGCACGCACGCACAGTAACTTCGTGCTGGGCAACCCCAGGTGGCGGGGCTCTTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   305 CGCTTCGACGGCACGCACGCACAGTAACTTCGTGCTGGGCAACCCCAGGTGGCGGGGCTCTTC 364

Qy   121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGTGACCTCACGGGTTCTCCGGGCTGAGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   365 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGTGACCTCACGGGTTCTCCGGGCTGAGGTC 424

Qy   181 ATGCAGCGCGGGCTGTGCCTGCTCTCTTTATGGCCAGACACCAGTGAGCTCGTCCGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   425 ATGCAGCGCGGGCTGTGCCTGCTCTCTTTATGGCCAGACACCAGTGAGCTCGTCCGC 484

Qy   241 CAACAGATCCGCAAGGCCCTGGACAGCAGCCCTGAGGCTCAAGGCTGAGCTGATCCTGTAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   485 CAACAGATCCGCAAGGCCCTGGACAGCAGCCCTGAGGCTCAAGGCTGAGCTGATCCTGTAC 544

Qy   301 CGGAAGAGCGGGCTCCGGTTCTGGTGTCTCTGGATGTGATACCCATAAAAGAATGAGAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   545 CGGAAGAGCGGGCTCCGGTTCTGGTGTCTCTGGATGTGATACCCATAAAAGAATGAGAAA 604

Qy   361 GGGGAGGTGGCTGCTCTCTCCTAGTCTCTCACAAGGACATCAGCGAACCAAGAACCGAGGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   605 GGGGAGGTGGCTGCTCTCTCCTAGTCTCTCACAAGGACATCAGCGAACCAAGAACCGAGGG 664

Qy   421 GGCCCCAGCAGATGGAAGAAGAGACAGGTGGTGGCGGAGACCGGCGACCGGCACGGATGC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   665 GGCCCCAGCAGATGGAAGAAGAGACAGGTGGTGGCGGAGACCGGCGACCGGCACGGATGC 724

Qy   481 AAAGGCTTCAATGCCAACCGCCGCGGGGAGCCGGGCCGCCGTCTCTACCACCTGTCCGGGAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   725 AAAGGCTTCAATGCCAACCGCCGCGGGGAGCCGGGCCGCCGTCTCTACCACCTGTCCGGGCAC 794

Qy   541 CTGCAGAAGCAGCCCAAGGCCAAGCACAACTCAATAAGGGGTGTTGGGGACAAACCA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   785 CTGCAGAAGCAGCCCAAGGCCAAGCACAACTCAATAAGGGGTGTTGGGGAGAAAACCA 844

Qy   601 AACTTGCCTGAGTACAAAGTAGCGCCATCCGGAAGTCGCCCTTCATCCGTTGCACTGT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   845 AACTTGCCTGAGTACAAAGTAGCGCCATCCGGAAGTCGCCCTTCATCCGTTGCACTGT 904

Qy   661 GGGGCACTGAGAGCCTACAGGCGTGTGTGAGCCACACGGGAGGACCGCCGTCTCTGCGGGCCCC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   905 GGGGCACTGAGAGCGCACCTGGGATGCCACCTGGGATGGCGGCACCGCCGTCTCTGCGGGCCCC 964

Qy   721 ACTGTGCCCTACAGGCGTGTGTGAGCGACACACGGGCCCTGGCCTGAGGCCCCTACAGCCCGGCCCTCTAC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   965 ACTGTGCCCTACAGGCGTGTGTGAGCGACACACGGGCCCTGGCCTGAGGCCCCTACAGCCCGGCCCTCTAC 1024

Qy   781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCCTTCATCCTGACATTGTGTCGAATTTC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1025 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCCTTCATCCTGACATTGTGTCGAATTTC 1084

Qy   841 CGTACCACCATTCGTGTCGCAAGTCGGCGTGGTGTTTGCCCAAAGTCCAITTGCCTC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 CGTACCACCATTCGTGTCGCAAGTCGGCGTGGTGTTTGCCCAAAGTCCAITTGCCTC   841

Db   1085 CGTACCACCATTCGTGTCGCAAGTCGGCGTGGTGTTTGCCCAAAGTCCAITTGCCTC 1144

Qy   901 CACTACGTCACCACCTGGTTCCTGCTGCTCTGCTGTGGGGCGTCTGGGGGCCATTCGTGCTGGGGCGTCTGGGGGCCATTCGACTGCTGCTA   960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1145 CACTACGTCACCACCTGGTTCCTGCTGCTCTGCTGGAIGTCATCGGAIGTCATCGGGACCTGCTA 1204

Qy   961 CAIGCCTTCAAGGTCAACGTGTACTTCGGGGCCCATTCGCTGGGGCCCATTCGCTGGGGCCCATTGCTGAAGACGTGCGCGCTGCTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1205 CATGCCTTCAAGGTCAACGTGTACTTCGGGGCCCATTGCTGCTGAAGACGTGCGCGCTGCTG 1264

Qy   1021 CGCCTGCTGCCCCTGCGTTCCGCCGGGTGGACCGAGCCTGACCGGTGACTGCGCAGGCGCGCCGTGGTGCTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CGCCTGCTGCCCCTGCGTTCCGCCGGGTGGACCGAGCCTGACCGGTGACTGCGCAGGCGCGCCGTGGTGCTG 1080

Db   1265 CGCCTGCTGCCCCTGCGTTCCGCCGGGTGGACCGAGCCTGACCGGTGACTACGGCGCGCCAGTACGGGCCGCAGTGTGCTG 1324

Qy   1081 ACACTGCTCATGGCCGTGTCCGCCTGCGCGCTGGCTGCCCACTGGGTCGCGGCGGGCACTGGTCTGGTTTAC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1325 ACACTGCTCATGGCCGTGTCCGCCTCTGCGCGGCCTCGGGCCGCCACTGGGTCGCGGCTGCCTGGTTTTAC 1384

Qy   1141 ATTGGCCAGCGGGAGATCGAGAGCAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGCTGCTGCAG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1385 ATTGGCCAGCGGGAGATCGAGAGCAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGCTGCTGCAG 1444

Qy   1201 GAGCTGGCGGCCCGGCTGGAGACTCCTGCGCGCAGCGCGCCTACATCACCTCCTTCTCCTCTACTTCGCACTC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1445 GAGCTGGCGGCCCGGCTGGAGACTCCTGCGCGCAGCGCGCCTACATCACCTCCTTCTCCTCTACTTCGCACTC 1504

Qy   1261 AACAGCTCGGCACAACTGCAGAGTGACAACTGCAGCAGCAGCCGCGGGAGCGAGCAGCCAACGGGAGCGGGCTG 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1505 AACAGCTCGGCACAACTGCAGAGTGACAACTGCAGCAGCAGCCGCGGGAGCGAGCAGCCAACGGGAGCGGGCTG 1564

Qy   1321 GAGCTGCTGGGCGCCCGTCGCTGCGCAGCGCTTCGACTTCCTCGCTCCCTCTACTTCGCACTC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1565 GAGCTGCTGGGCGCCCGTCGCTGCGCAGCGCTTCGACTTCCTCGCTCCCTCTACTTCGCACTC 1624

Qy   1381 AGCAGGCTCACCAGCGGTGGCGTTCGGCTTCGGCAACGTGCTCGGCAACGTGCTCGGGACACCGAGAAGATC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1625 AGCAGGCTCACCAGCGGTGGCGTTCGGCTTCGGCAACGTGCTCGGCAACGTGCTCGGGACACCGAGAAGATC 1684

Qy   1441 TTCTCCATCTGCACCATGCTCATCTCTGACCGGTGGCACGCGGTGGTGTTTGGGGAACGTG 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1685 TTCTCCATCTGCACCATGCTCATCTCTGACCGGTGGCACGCGGTGGTGTTTGGGGAACGTG 1744

Qy   1501 ACGGCCATCATCCAGCGACATCCAGCCATGTGACGCCCGCGTTTCTGTTCTGTCACAGGCCGACGGCGCGAC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1745 ACGGCCATCATCCAGCGACATCCAGCCATGTGACGCCCGCGTTTCTGTTCTGTCACAGGCCGACGGCGCGAC 1804

Qy   1561 CTGCGGCACTACATCCCAICGCGATCCCGGIATCCCGGIATCCCCTCAAGCAGCCCATGCTGGAG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1805 CTGCGGCACTACATCCCAICGCGATCCCGGIATCCCGGIATCCCCTCAAGCAGCCCATGCTGGAG 1864

Qy   1621 TACTTCCAGGCCACCTGGGCGGTGAACAATGGCATCAGCACCGGGAGGCTGCTGCGAGAGC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1865 TACTTCCAGGCCACCTGGGCGGTGAACAATGGCATCAGCACCGGGAGGCTGCTGCGAGAGC 1924

Qy   1681 CTCCCTGACGAGCTGCGGCGCAGACATCGCCATGCCATGCCATCGCCACCTGCACCAGCTG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1925 CTCCCTGACGAGCTGCGGCGCAGACATCGCCATGCCATGCCATCGCCACCTGCACCAGCTG 1984

Qy   1741 CCACTGTTTGAGCGGCGCCGGAGCTGCTGCCTGCGGGCACTGTCTCTGGCCCCGCGGCCC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1985 CCACTGTTTGAGCGGCGCCGGAGCTGCTGCCTGCGGGCACTGTCTCTGGCCCCTGCGGGCCCC 2044

Qy   1801 GCCTTCTGCACGCGGGGCGAGTACCTCATCCACCAAGGCGATGCCGTGCTCTGCTGCCGATCTCCTAC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2045 GCCTTCTGCACGCGGGGCGAGTACCTCATCCACCAAGGCGATGCCGTGCTGCTGCCCCTCTAC 2104

Qy   1861 TTTGTCTGCTCTGGCTCTGGCCGTGGTGACCTGGCCACCGTGCTCAAGGGTGGCACCGTGCTCAAGGGTGGCCATCCTAGGG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2105 TTTGTCTGCTCTGGCTCTGGCCGTGGTGACCTGGCCACCGTGCTCAAGGGTGGCACCGTGCTCAAGGGTGGCCATCCTAGGG 2164

Qy   1921 AAGGGCGACCTGATCGGCTGGTGAGCTGTGAGCTGCCCCGGGCGGGGAGCAGGTGGTAAAGGCCAATGCC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2165 AAGGGCGACCTGATCGGCTGGTGAGCTGTGAGCTGCCCCGGGCGGGGAGCAGGTGGTAAAGGCCAATGCC 2224

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Qy   1981  GACGTGAAGGGCTGACTACTGCGTCCTGCAGTGTCTGCAGCTGTCGCAGCTGCGACGAC  2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2225  GACGTGAAGGGCTGACGTACTGCGTCCTGCAGTGTCTGCAGCTGTCGCAGCTGCGACGAC  2284

Qy   2041  AGCCTTGCGCTGTACCCCGAGTTGCCCCGCGCTTCAGTCGTGGCCTCGGAGGGGAGCTC  2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2285  AGCCTTGCGCTGTACCCCGAGTTGCCCCGCGCTTCAGTCGTGGCCTCCGAGGGGAGCTC  2344

Qy   2101  AGCTACAACCTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCAGTTCCTGAGCGGC  2160
           ||||||||||||||||||||||| |||||||||||||||||||||| || |||
Db   2345  AGCTACAACCTGGGTGCTGGGGAGGCTCTGCAGAGGTGGACACCAGCTCCTGAGCGGC  2404

Qy   2161  GACAATACCCTTATGTCCACGCTGGAGGAGACAGATGGGGAGCAGGGCCCCACG  2220
           |||||||||| |||| |||||||||||||||||||||||||||||||||||
Db   2405  GACAATACCCTTATGTCCACCCTGGAGGAGGAGACAGATGGGGAGCAGGGCCCCACG  2464

Qy   2221  GTCTCCCCAGCCCCCAGCTGATGAGCCCTGCTGTCCCCGGCCTCGTCTAGGT  2280
           ||||||| ||||||||| || ||||||||||||||| |||||||||
Db   2465  GTCTCCCCAGCCCCCAGCTGATGAGCCCTGCTGTCCCCTGCCTCGTCTAGGT  2524

Qy   2281  TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTGAACAGCACCCCGGCCTCGTCTAGGT  2340
           |||||||||||||||||||||||||||| |||||||||||||||||||| |||||||
Db   2525  TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTGAACAGCACCCCGGCCTCGTCTAGGT  2584

Qy   2341  GGCAGAGGGAGGGCCAGGCAGGGCAGGGCAGGGCTTTGAAGGCTGAGGTGCCCCTCTGCTCCC  2400
           |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   2585  GGCAGAGGGAGGGCCAGGCAGGGCAGGGCAGGGCTTTGAAGGCTGAGGTGCCCCTGTGCTCCC  2644

Qy   2401  CCACGGGCCCTAGAGGGCTACGGGTGCCCCCGGAATGTGCCCCCAGATCTG  2460
           |||||||||||||||||| |||||||||||||||||||||||||||||||
Db   2645  CCACGGGCCCTAGAGGGCTACGGGTGCCCCCGGAATGTGCCCCCAGATCTG  2704

Qy   2461  AGCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGAACCAAGTTCTCT  2520
           ||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   2705  AGCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGAACCAAGTTCTCT  2764

Qy   2521  TTCGGCGGTGGGCCAGTCTGCCCCGAATGTAGCAGCAGCCCCTGCCCCTGACCAGAGAGC  2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2765  TTCGGCGGTGGGCCAGTCTGCCCCGAATGTAGCAGCAGCCCCTGCCCCTGACCAGAGAGC  2824

Qy   2581  GGCCTGCTCACTGTTCCCCATGGGCCCAGCGCCGAGGCAAGGAACACACAGCTGGACAAG  2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2825  GGCCTGCTCACTGTTCCCCATGGGCCCAGCGCCGAGGCAAGGAACACACAGCTGGACAAG  2884

Qy   2641  CTTCGGCAGGCGGTGACAGAGCTGTCGCAGGTGCTGCAGACTGCGGGGAAGGACTGCAG  2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2885  CTTCGGCAGGCGGTGACAGAGCTGTCGCAGGTGCTGCAGACTGCGGGGAAGGACTGCAG  2944

Qy   2701  TCACTTCGGCAGGCTGTGCAGCTTGTCCTGGCCCCACAGGGAGGTCCGTGCCCTCGG  2760
           ||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   2945  TCACTTCGGCAGGCTGTGCAGCTTGTCCTGGCCCCACAGGGAGGTCCGTGCCCTCGG  3004

Qy   2761  GCATCGGCGGAGAGGGGCCGTGCCCAGCGAACCTCCGGGCTTCTGCAGCCTCTGTGTGTG  2820
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3005  GCATCGGCGGAGAGGGGCCGTGCCCAGCGAACCTCCGGGCTTCTGCAGCCTCTGTGTGTG  3064

Qy   2821  GACACTGGGGCATCCTCCTACTGCCCCGAGCCCCAGCTGCTGTCTGTCTTGAGTGGGACT  2880
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3065  GACACTGGGGCATCCTCCTACTGCCCCGAGCCCCAGCTGCTGTCTGTCTTGAGTGGGACT  3124

Qy   2881  TGGCCCCACCCTGTCCGGGCCTCCTCCCTCATGGCACCCTGGGTCCCCCA  2940
           ||||||||||||||||||||||| |||||||||||||||||||||||||
Db   3125  TGGCCCCACCCTGTCCGGGGCCTCCTCCATGGCACCCTGGGTCCCCCCA  3184

Qy   2941  GCGTCTCAGAGCTCCCCCTGGCCTGACCTGGACACCTTCTGCAACCTCCACCTCA  3000
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   3185  GCGTCTCAGAGCTCCCCCTGGCCTGACCTGGACCACCTTCTGACCTCCACCTCA  3244

Qy   3001  GAGCCCCTGCCTCGTCTGAGCGAGACCTCTGAGCCCAGCACCCCTGCCTCCCTCCTCC  3060
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db   3245  GAGCCCCTGCCTCGTCTGAGCGAGACCCTCTGAGCCCAGCACCCCTGCCTCCCTCCTCCT  3304
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Qy   3061  TCTGAGGAAGGGGCTAGGACTGGGCCCGCAGAGCCTGTGAGCGAGGCTACCAGC  3120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3305  TCTGAGGAAGGGGCTAGGACTGGGCCCGCAGAGCCTGTGAGCGAGGCTACCAGC  3364

Qy   3121  ACTGGAGAGCCCCCACCAGGTCAGGGGGCTCAGGGGCCTGGCCCTGGACCCCACAGCCTG  3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3365  ACTGGAGAGCCCCCACCAGGTCAGGGGGCTCAGGGGCCTGGCCCTGGACCCCACAGCCTG  3424

Qy   3181  GAGATGGTGCTTATTGGCTGCCATGCTGTCTGGCACAGTCAGTGGACCCAGGAAGAAGGC  3240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3425  GAGATGGTGCTTATTGGCTGCCATGCTGTCTGGCACAGTCAGTGGACCCAGGAAGAAGGC  3484

Qy   3241  ACAGGGGTCTGA  3252
           ||||||||||||
Db   3485  ACAGGGGTCTGA  3496
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RESULT 3
AA250119
ID   AA250119 standard; cDNA; 3249 BP.
XX
AC   AA250119;
XX
DT   04-MAY-2000 (first entry)
XX
DE   Human Elk voltage gated potassium channel monomer encoding cDNA.
XX
KW   voltage gated potassium channel subunit; VGPCs; hElk; human; stroke;
KW   Kv superfamily; Eag family; ether a go-go; Elk subfamily; modulator;
KW   chromosome 12q13; resting potential; cell excitability; seizure;
KW   CNS; migraine; psychotic; anticonvulsant; ion flux disorder; detection;
KW   gene therapy; antimigrane; cerebroprotective; neuroprotective;
KW   antipsychotic; ss.
XX
OS   Homo sapiens.
XX
FH   Location/Qualifiers
FT   Key
FT   mat_peptide   1..3249
FT   /tag= a
FT   /product= "Human Elk polypeptide"
FT   /note= "Alpha subunit of voltage gated potassium channel
FT   monomer"
FT   /transl_except= (pos:2893..2895, aa:Ala)
XX
PN   WO200001819-A1.
XX
PD   13-JAN-2000.
XX
PF   30-JUN-1999; 99WO-US14944.
XX
PR   01-JUL-1998; 98US-0091469.
PR   21-JAN-1999; 99US-0116621.
XX
PA   (ICAG-) ICAGEN INC.
XX
PI   Jegla TJ, Wickenden A;
XX
DR   WPI; 2000-182114/16.
DR   P-PSDB; AAY44778.
XX
PT   Novel polynucleotides and polypeptides of human ELK, a voltage-gated
PT   potassium channel subunit useful for treating ELK mis-expression and
PT   to screen for inhibitors and activators of such channels -
XX
PS   Claim 4; Page 62-64; 79pp; English.
XX
CC   The present sequence is the cDNA encoding human ELK (hElk) polypeptide
CC   monomer, comprising an alpha subunit of the voltage-gated potassium
CC   channel (VGPCs). It is a member of the Kv (voltage gated potassium)
CC   superfamily, Eag (ether a go-go) family and Elk subfamily of potassium
CC   channel monomers. hElk gene is mapped to chromosome 12q13. It is isolated
CC   from brain and maintains the resting potential and controls excitability,
CC   of the cell. It has antimigrane, cerebroprotective, antipsychotic,

```
CC   neuroprotective and anticonvulsant activity. The RELk polypeptide can be
CC   used to screen for modulators of VGPCs, that are useful for treating
CC   abnormal ion flux disorders, CNS disorders such as migraines, hearing
CC   and vision problems, seizures, psychotic disorders and to prevent
CC   strokes. It can be used as a marker for diagnosis of diseases linked to
CC   this gene and also as reporter molecule in detection systems. The
XX   polynucleotide is useful for gene therapy, to rectify ELK expression.
SQ   Sequence 3249 BP; 562 A; 1097 C; 1000 G; 590 T; 0 other;

Query Match             99.8%;  Score 3245.8;  DB 21;  length 3249;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 3247;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;
```

```
Qy      1 ATGCGGCCATGCGGGGCCTTCCTGGCGCCCAGTGAACACCTTCCTGGACACCATCGCTACG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGCGGCCATGCGGGGCCTTCCTGGCGCCCAGTGAACACCTTCCTGGACACCATCGCTACG 60

Qy     61 CGCTTCGACGGCCACGCCACCAGTAACTTCTGTCTGCTCTGTGACCTTCTCTGTGAGGTC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CGCTTCGACGGCCACGCCACCAGTAACTTCTGTCTGCTCTGTGACCTTCTCTGTGAGGTC 120

Qy    121 CCCGTGGTCTCACTGCTCTGATGGCTTCTCTGTGACCTTCTCCGGGCTTCTCCCGGGGTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCGTGGTCTCACTGCTCTGATGGCTTCTCTGTGACCTTCTCCGGGCTTCTCCCGGGGTC 180

Qy    181 ATGCAGCGGGGCTGTGCTGCTGCTTTATGGGCCAGACACCAGTCGTCCGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATGCAGCGGGGCTGTGCTGCTGCTTTATGGGCCAGACACCAGTCGTCCGC 240

Qy    241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGAGCTCGATCCTGTAC 300
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Qy    301 CGGAAGAGCGGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGAAGAGCGGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA 360

Qy    361 GGGGAGGTGGCTCTCTTCCTAGTCTCTCACAAGGACACAAGGAGTTCAAGGCCGAGGG 420
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Qy    421 GGCCCCGACGACAATGGAAGGAAGAGCAGTGGTGGCCGGCGATATGGCCGGCACGATCC 480
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Db    421 GGCCCCGACGACAATGGAAGGAAGAGCAGTGGTGGCCGGCGATATGGCCGGCACGATCC 480

Qy    481 AAAGGCTTCAATGCAAAGTAGCCGGCATCCGGCGTCCTGCTCTACCGCCTGTCCGGCCAC 540
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Db    481 AAAGGCTTCAATGCAAAGTAGCCGGCATCCGGCGTCCTGCTCTACCGCCTGTCCGGCCAC 540

Qy    541 CTGCAGAAGCAGCCCAAGGCCAAGAGCAACAGCAAGGGGGTGTTGGGGAGAAACCA 600
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Db    541 CTGCAGAAGCAGCCCAAGGCCAAGAGCAACAGCAAGGGGGTGTTGGGGAGAAACCA 600

Qy    601 AACTTGCCTGAGTACAAAGTAGCCGGCACATCCGGAAGTCGCCCTTCATCCTGTGCACTGT 660
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Db    601 AACTTGCCTGAGTACAAAGTAGCCGGCACATCCGGAAGTCGCCCTTCATCCTGTGCACTGT 660

Qy    661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCGTCTCGCCACACTCTATGTGGCTGTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    721 ACTGTGCCCTACAGGGTGTGTGAGCACAGCACCGAGGCCAGTGCGCCCCCGCCCCCCG 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    781 CCCAGCGTCTGTGACCTGGAGGTCCTCTCATCCTGACCTCATGTGCTGAATTGC 840
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Qy    841 CGTACCACATTCGTGTCCAAGTCGGGCCAGGTGGTTGCCCCAAAGTCCATTGCCTC 900
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Qy    901 CACTACGTCACCACCTGGTCCTCCTGCTGATGTCATCGGATGTCATCGACGCGTCATC 950
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACTACGTCACCACCTGGTCCTCCTGCTGATGTCATCGGATGTCATCGACGCGTCATC 950

Qy    961 CATGCCTTCAAGTCAACGTCAACCTGTACTTCGGGGCCCATCGCTGAAGCGGTGCCGTCTGCTG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1021 CGCCTGCTGCGCGCCTGCTTCCGCCGCCTGGACCGGCTACTCGCAGTACAGGCCGTGGTGCTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CGCCTGCTGCGCGCCTGCTTCCGCCGCCTGGACCGGCTACTCGCAGTACAGGCCGTGGTGCTG 1080

Qy   1081 ACACTGCTCATGGCCGTGTTCGCCGCCACTGGGTCCCGCACTGGGTCTCGGTTTAC 1140
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Qy   1321 GAGCTGCTGGGGCGGCCCGTGCTCGCCTGCGCAGGCCTCACATCACCTCCGCTACTTCGGCACTC 1380
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Qy   1621 TACTTCCAGGCCATCAGGCCGGTGAACAATGGCATCCGACCACCGAGTGCTGCGAGAGC 1680
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Db   1621 TACTTCCAGGCCATCAGGCCGGTGAACAATGGCATCCGACCACCGAGTGCTGCGAGAGC 1680

Qy   1681 CTCCCTGACGAGCTGCGCCGCAGAGCTGCCCAGAGACACATCGCCACTGCAAGGAGGTCCAGCTG 1740
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Qy   1741 CCACTGTTTGAGGGCGCTCTCGGCCTGCGCCCTGACGGGATGCCTGCCAGGCCGGCCCTCTAC 1800
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Db   1741 CCACTGTTTGAGGGCGCTCTCGGCCTGCGCCCTGACGGGATGCCTGCCAGGCCGGCCCTCTAC 1800

Qy   1801 GCCTTCTGCAGCTGCGCCTCATCCTGCCGCTGCCTGCGGCACTGTGCTCCGGCCCATCCTAGGG 1860
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Db   1801 GCCTTCTGCAGCTGCGCCTCATCCTGCCGCTGCCTGCGGCACTGTGCTCCGGCCCATCCTAGGG 1860

Qy   1861 TTTGTCTGCTCTGCCTCGGCAGGTGTCATGGAGGTCAAGGTGCTGCTCGGCACCGTGCTGGG 1920
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Db   1861 TTTGTCTGCTCTGCCTCGGCAGGTGTCATGGAGGTCAAGGTGCTGCTCGGCACCGTGCTGGG 1920

Qy   1921 AAGGGCGACCTGATCGGCTCGTGTCCAAGTCGGGCCGGGAGCGGAGGTGGTAAAGGCCAATGCC 1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 AAGGGCGACCTGATCGGCTCGTGTCCAAGTCGGGCCGGGAGCGGAGGTGGTAAAGGCCAATGCC 1980
```

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Qy   1981  GACGTGAAGGGCTGACGTACTGCGTCCTGCTGCAGCTGTCTGCAGTGTCTGCAGCTGGCCTGCGCCGCACGAC 2040
           ||||||||||||||||||||||||||| ||||||  ||||||||||||||||||||||| ||||||| ||||
Db   1981  GACGTGAAGGGCTGACGTACTGCGTCCTGCTGCAGCTGTCTGCAGTGTCTGCAGCTGGCCTGCGCCGCACGAC 2040

Qy   2041  AGCCTTGCGCTGTACCCCGAGTTTGCCCCGCCTTCAGTCGTGGCCTTCGCGAGGGGAGCTC 2100
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           |||||||| ||||||||||||||||||||||||||||||   ||||||||||
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Qy   2341  GGCAGAGGGAGGAGGCCAGGCAGGCAGGGCTTTGAAGGCTGAGGCTGGCCCCTTGCTCCC 2400
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Qy   2401  CCACGGGCCCTAGAGGGGCTACGGGTGCCCCCCATGGCATGGAATGTGCCCCCAGATCTG 2460
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Db   2401  CCACGGGCCCTAGAGGGGCTACGGGCGCCCCCCATGGCATGGAATGTGCCCCCAGATCTG 2460

Qy   2461  AGCCCCAGGGTAGTAGAATGGCATTGAAGACGGCTGTGGCTCGGACCAGCCCAAGTTCTT 2520
           ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   2461  AGCCCCAGGGTAGTAGAATGA-GGCATTGAAGACGGCTGTGGCTCGGACCAGCCCAAGTTCTCT 2520

Qy   2521  TTCCGCGTGGGCCAGTCTCGGCCCCGGAATGTAGCAGCAGCCCCTCCCCTGGACACAGAGAGC 2580
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Qy   2581  GGCCTGCTCACTGTTCCCCATGGGCCCAGCGAGGCAAGGAACACAGAACACACTGGACAAG 2640
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Db   2581  GGCCTGCTCACTGTTCCCCATGGGCCCAGCGAGGCAAGGAACACAGAACACACTGGACAAG 2640

Qy   2641  CTTCGGCAGCGGTGACAGAGCTTGCAGCTGCTGCAGATGCGGGAAGGACTGCAG 2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  CTTCGGCAGCGGTGACAGAGCTTGCAGCTGCTGCAGATGCGGGAAGGACTGCAG 2700

Qy   2701  TCACTTCGCCAGGCTGTGCAGCTTGTCCTGCGGCAGCTTCCGTGCCCTGGG 2760
           ||||||||||||||||||||| |||||||||||||||||| |||||||||
Db   2701  TCACTTCGCCAGGCTGTGCAGCTTGTCCTGCGGCAGCTTCCGTGCCCTCGG 2760

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           ||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   2761  GCATCGGGAGAGGGGCCGTGCCCAGCAGCACCTTCTGCAGCCTCTGTGTGTG 2820

Qy   2821  GACACTGGGCCATCCTCCTACTCGCTGCAGCCCCCAGCTGGCCTG 2880
           ||||||||||||||||||||||||||||||||||||||||||||
Db   2821  GACACTGGGCCATCCTCCTACTCGCTGCAGCCCCCAGCTGGCCTG 2880

Qy   2881  TGGCCCCACCCTGTCTCCGGGGGCTCGGGGGTCCCCCA 2940
           ||||||||||||||||||||||||||||||||||||||
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Qy   2941  GCGTCTCAGAGCTCCCCCTGCCTCGACCTCACCTCAGACTCA 3000
           ||||||||||||||||||||||||||||||||||||||||||
Db   2941  GCGTCTCAGAGCTCCCCCTGCCTCGACCTCACCTCAGACTCA 3000

Qy   3001  GAGCCCCTGCCTCTGCTCTCGGAGCACCCTGCCTCCCCTCCT 3060
           |||||||||||||||||||||||||||||||||||||||
Db   3001  GAGCCCCTGCCTCTGCTCTCGGAGCACCCTGCCTCCCCTCCT 3060

Qy   3061  TCTGAGGAGGGGCTAGGACTGGCCCGAGACGCTGTGAGCCGCTGAGGCTACCAGC 3120
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Db   3061  TCTGAGGAGGGGCTAGGACTGGCCCGAGAGCCTGTGAGCCGCTGAGGCTACCAGC 3120

Qy   3121  ACTGGAGAGCCCCACCAGGGTCAGGGGGCCTGGCCCTTGCCCTGGGACCCCCACAGCCTG 3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3181  GAGATGTGCTTATTGGCTGCCATGGCTCTGGCCACAGTCCAGTGGACCCAGGAAGAGGC 3240
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Db   3181  GAGATGTGCTTATTGGCTGCCATGGCTCTGGCCACAGTCCAGTGGACCCAGGAAGAGGC 3240

Qy   3241  ACAGGGGTC 3249
           |||||||||
Db   3241  ACAGGGGTC 3249
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RESULT 4
AAA14893
ID   AAA14893 standard; DNA; 3252 BP.
XX
AC   AAA14893;
XX
DT   08-AUG-2000 (first entry)
XX
DE   DNA encoding a herg4, potassium channel protein of the ERG family.
XX
KW   Human; potassium channel protein; Herg4; human erg related gene 4;
KW   epilepsy; migraine; cell proliferation disorder; cancer;
KW   comportemental trouble; neurotransmitter; hormone; ischemia;
KW   brain disease; cardiac disease; inflammation; pain; ss.
XX
CS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..3252
FT   /tag= a
FT   /product= "human erg related gene 4"
XX
PN   WO200022001-A2.
XX
PD   20-APR-2000.
XX
PF   13-OCT-1999; 99WO-EP07671.
XX
PR   13-OCT-1998; 98EP-0402540.
XX
PA   (SNFI) SANOFI-SYNTHELABO.
XX
PI   Renard S, Avenet P;
XX
DR   WPI; 2000-317948/27.
DR   P-PSDB; AAY84835.
XX
PT   Novel herg4 polypeptide of human erg potassium channel family useful
PT   for treatment of epilepsy, migraine, cell proliferation -
XX
PS   Claim 5; Page 41-45; 48pp; English.
XX
CC   The present sequence encodes a human potassium channel protein of
CC   the ERG family, which is designated Herg4 (human erg related gene 4).
CC   The Herg4 polypeptides and polynucleotides are useful in the treatment
CC   of epilepsy, migraine, cell proliferation disorders, cancer,
CC   comportemental troubles, and to prevent or alter the effect of
CC   endogenous neurotransmitters and hormones. Antibodies against
CC   Herg4 are also useful for the treatment of cerebral, cardiac and renal
CC   ischemias, brain and cardiac diseases, inflammation, pain, and to mimic
CC   or antagonize the effect of endogenous neurotransmitters and hormones.
XX
SQ   Sequence 3252 BP; 562 A; 1099 C; 1000 G; 591 T; 0 other;

Query Match   99.8%;   Score 3244;   DB 21;   Length 3252;
Best Local Similarity 99.8%;   Pred. No. 0;
Matches 3247; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy   1081 ACACTGCTCATGGCCGTGTTCGCCCTGCTCGGCGACACTGGGTCGGTCGCTCGGTTTTAC 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ACACTGCTCATGGCCGTGTTCGCCCTGCTCGGCGACACTGGGTCGGTCGCTCGGTTTTAC 1140

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATTGGCCAGCGGGAGATCGAGAGCACCGAGATCCGAGTTGCTGAGATTGGCTGGCTGCAG 1200

Qy   1201 GAGCTGGCCCGCACTGGAGACTCCCTACTACCTCGGTGGGCCGGAGGCCAGCTGGAGGG 1260
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Db   1201 GAGCTGGCCCGCACTGGAGACTCCCTACTACCTCGGTGGGCCGGAGGCCAGCTGGAGGG 1260

Qy   1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCGAGCCAACGGACGGGGGCTG 1320
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Db   1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCGAGCCAACGGACGGGGGCTG 1320

Qy   1321 GAGCTGCTGGCGGCCCGCTGCTGCGCAGCGGCCTCACTTCGGACTTCGCACTC 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1381 AGCAGCCTCACCAGCGTGGGCTTCGGCAACGTGTCCGGCAACACCGAGAAGATC 1440
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Db   1381 AGCAGCCTCACCAGCGTGGGCTTCGGCAACGTGTCCGGCAACACCGAGAAGATC 1440

Qy   1441 TTCTCCAICTGCACCATGCTCATGGCGGCCCTGATGCGACGCGGGTGTTGGGAACGTG 1500
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Db   1441 TTCTCCATCTGCACCATGCTCATGGCGGCCCTGATGCGACGCGGGTGTTGGGAACGTG 1500

Qy   1501 ACGGGCCATCATCCAGGCGATGTACGCCCGGCGCTTCGTACCACAGGCGCACGCGGCGAC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 ACGGGCCATCATCCAGGCGATGTACGCCCGGCGCTTCGTACCACAGGCGCACGCGGCGAC 1560

Qy   1561 CTGCGGCGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAGCAGCCATGCTGGAG 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1681 CTCCCTGACGAGCTGCGCGCAGACATCGCCATGCCATCGCACCTGCACAAGGAGTCCTGCAGCTG 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CTCCCTGACGAGCTGCGCGCAGACATCGCCATGCCATCGCACCTGCACAAGGAGTCCTGCAGCTG 1740

Qy   1741 CCACTGTTTGAGGCGGGCCACTGTGAGCCGCCTCGTCTCTGTCGGCCCTCGCCCC 1800
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Db   1741 CCACTGTTTGAGGCGGGCCACTGTGAGCCGCCTCGTCTCTGTCGGCCCTCGCCCC 1800

Qy   1801 GCCTTCTGCACGGCGGGCGACGTACTGCGCTCCATCCCACCAAGGCGATGCCCTCAGCAGC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GCCTTCTGCACGGCGGGCGACGTACTGCGCTCCATCCCACCAAGGCGATGCCCTCAGCAGC 1860

Qy   1861 TTTGTCTGCTCTGGCTTCATGGAGGTGCTCAAGGGTGGCACGGTGGCCTCCCATCCTAGGG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 TTTGTCTGCTCTGGCTTCATGGAGGTGCTCAAGGGTGGCACGGTGGCCTCCCATCCTAGGG 1920

Qy   1921 AAGGGCCACCTGATCGGCTGCGTGAGCTGTGAGCCGGGAGCCAGTGGTAAAGGCCAATGCC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 AAGGGCCACCTGATCGGCTGCGTGAGCTGTGAGCCGGGAGCCAGTGGTAAAGGCCAATGCC 1980

Qy   1981 GACGTGAAGGGGCTGACGTACTGCGTCCGCAGTCGTCCTCGCGGCTGGCGCACGAC 2040
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Db   1981 GACGTGAAGGGGCTGACGTACTGCGTCCGCAGTCGTCCTCGCGGCTGGCGCACGAC 2040

Qy   2041 AGCCTTGCGCTGTACCCCGAGTTTGCCCGCGCTTCAGTCGTGCGCGTTCCGAGGGAGCTC 2100
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Qy   2101 AGTACAAACCTGGTGTCGTGGGGGAGGCTCTGCAGGAGGTGTCGGACACCGGT 2160
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Db   2101 AGTACAAACCTGGTGTCGTGGGGGAGGCTCTGCAGGAGGTGTCGGACACCGGC 2160

Qy   2151 GACAATACCCTATGTCCACGCTGGAGGAGAAGGAGAGACAGATGGGGAGCAGGGCCCACG 2220
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Qy      1 ATGCCGGGCCATGGGGGGCTCCTGCGGCCGCTCAGAACACGTTCCTGGACACCACCGTACG 60
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Db      1 ATGCCGGGCCATGGGGGGCTCCTGCGGCCGCTCAGAACACGTTCCTGGACACCACCGTACG 60

Qy     61 CGCTTCGACGGCACGCACCGCAGCGTAACTTCGTGCTGGGCAACGCGCCAGTGGCGGGCTTTTC 125
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CGCTTCGACGGCACGCACCGCAGCGTAACTTCGTGCTGGGCAACGCGCCAGTGGCGGGCTCTTC 120

Qy    121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGCTTCTCCCGGGCTGAGGTC 180
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Qy    181 ATGCAGGGGGCTGTGCCTCTCCTTCCTTATGGCCAGACCCACTGAGCTCGTCCGG 240
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Qy    241 CAACAGATCCGCACGGCCCTTGGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    301 CGGAAGAGCGGGGGCTCCCGGTCTGGTTCTCTGTCTCCTGGATGTGATACCCATAAAGATGAGAAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGAAGAGCGGGGGCTCCCGTTCTGGTTCTCTGTCTCCTGGATGTGATACCCATAAAGATGAGAAA 360

Qy    361 GGGGAGGTGGCCTCTTCTTCCTCTAGTCTCTCACCAAGGACTCAGCGGAACCAAGAAACCGAGG 420
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Db    361 GGGGAGGTGGCCTCTTCTTCCTCTAGTCTCTCACCAAGGACTCAGCGGAACCAAGAAACCGAGGG 420

Qy    421 GGCCCGACAGATGAAGGAGACAGTGGTGCCGGGGCCGTGGTCTCTACCACCGTCCGGGCCAC 480
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Qy    541 CTGCGAAGCAGCAGCCCAAGCACAAGCTCAAGCTCAATCCGGAAGTCGCCCCTTCATCCTGTTGCACTGT 600
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Db    541 CTGCGAAGCAGCAGCCCAAGCACAAGCTCAATCCGGAAGTCGCCCCTTCATCCTGTTGCACTGT 600

Qy    601 AACTTGCCTGGATTCTGGGATGGCTTCATCCTGCTCCGCCTCTCGCCGTCTCCTGTTGCACTGT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACTTGCCTGGATTCTGGGATGGCTTCATCCTGCTCCGCCTCTCGCCGTCTCCTGTTGCACTGT 660

Qy    661 GGGGCACTGAGAGCCACCTGGATGGCTTCATCCGCCTCTCGCCCACACTCTATGTGGCCGTC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GGGGCACTGAGAGCCACCTGGATGGCTTCATCCGCCTCTCGCCCACACTCTATGTGGCCGTC 720

Qy    721 ACTGTGCCCTACACCAGGCGTGTGTGAGCACACGAGCAGCCCAGTCACGCGGGCCG 780
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Qy    781 CCCAGCGTCTGTGACCTGGCGTGAGGTCCATCCTTCTTCCTTGACATTGTGTCGAATTC 840
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Qy    841 CGTACCACATTCGTGTCCAAGTCGGCGTCCCAGGTGGTGTTTGCCCCAAAGTCCATTTGCCTC 900
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Qy    901 CACTACGTCACCACCTGGTTCCTGCTGGATGTCATCGGGCCCATCCTGAAGACGCTGCCCTTTGACCTGTA 960
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Db    901 CACTACGTCACCACCTGGTTCCTGCTGGATGTCATCGGGCCCATCCTGAAGACGCTGCCCTTTGACCTGCTA 960

Qy    961 CATGGCCTTCAAGGTCAACGTGTACTTCGGGGCCATCCGTGCTCGAAGACGGTGCCCGCCTGGTCGGTG 1020
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Db    961 CATGGCCTTCAAGGTCAACGTGTACTTCGGGGCCATCCGTGCTCGAAGACGGTGCCCGCCTGGTCGGTG 1020

Qy   1021 CGCCTGCTGCCCTGCTTCCCGGCGGCTGCGACCGGCTACTCCGCAGTGACACGCGCCGTGGTGCTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CGCCTGCTGCCCTGCTTCCCGGCGGCTGCGACCGGCTACTCCGCAGTGACACGCGCCGTGGTGCTG 1080
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Db   3241 ACAGGGGTCTGA 3252

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Db                          3241 ACAGGGTCTGA 3252

RESULT 5
AAZ11906
ID   AAZ11906 standard; cDNA; 3857 BP.
XX
AC   AAZ11906;
XX
DT   30-NOV-1999 (first entry)
XX
DE   Human potassium channel K+Hnov14 cDNA.
XX
KW   Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW   cardiovascular disorder; CNS disorder; renal disorder; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             249..3497
FT                   /tag= a
FT                   /product= "Human K+Hnov14 potassium channel"
FT   variation       replace (3158,T)
FT                   /tag= b
XX
PN   WO9943696-A1.
XX
PD   02-SEP-1999.
XX
PF   22-FEB-1999; 99WO-US03826.
XX
PR   19-JAN-1999; 99US-0116448.
PR   25-FEB-1998; 98US-0076687.
PR   07-AUG-1998; 98US-0095836.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Curran ME,  Hu P,  Miller AP,  Rutter M,  Wang J;
XX
DR   WPI; 1999-527591/44.
DR   P-PSDB; AAY34128.
XX
PT   New nucleic acids encoding mammalian K+Hnov potassium channel.
PT   proteins, useful for the diagnosis and treatment of episodic ataxia
PT   with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
XX
PS   Claim 4; Page 72-76; 112pp; English.
XX
CC   This sequence represents human potassium channel K+Hnov14 cDNA.
CC   K+Hnov proteins have a high degree of homology to known potassium
CC   channels and may be alpha subunits, which form the functional channel,
CC   or accessory subunits that act to modulate the channel activity.
CC   K+Hnov14 is a 6 transmembrane domain, voltage gated potassium channel.
CC   The gene's chromosomal location is 12q14, determined via PCR
CC   chromosomal localisation using primers AAZ11928 and AAZ11929.
CC   K+Hnov cDNAs were isolated by extension of expressed sequence tags
CC   (ESTs) which were related but not identical to known human potassium
CC   channels. Potential polymorphisms detected as sequence variants between
CC   multiple independent clones. Potassium channels have critical roles in
CC   various cell types and biochemical pathways. Defective potassium channels
CC   are known to cause four human diseases: episodic ataxia with myokymia;
CC   cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
CC   As potassium channels are critical components of virtually all cells,
CC   it is likely that abnormal potassium channels are also implicated in
CC   certain renal, cardiovascular and central nervous system (CNS)
CC   disorders. Nucleotides encoding K+Hnov proteins may be used for
CC   identifying homologous or related proteins and the DNA sequences encoding
CC   them. They may be used to produce compositions that modulate the
CC   expression and function of the K+Hnov protein and in studying the
CC   biochemical pathways associated with it. They may also be used for the
CC   recombinant production of K+Hnov protein in fermentation cultures.
CC   Additionally, such nucleotides may be used in gene therapy protocols for
CC   the treatment of diseases associated with abnormal potassium channels.
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Qy  2161 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GACAATACCCTTATGTCACGCTGGAGGAGAAGGAGACAGATGGGGAGCAGGGCCCCACG 2220
Db  2221 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GTCTCCCCAGCCCCAGCTGATGAGCCCTCAGCCCCGTCGTGTCCCCTGGCTGCACCTCC 2280

Qy  2221 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCGTCGTCCCCTGGCTGCACCTCC 2280
Db  2281 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2281 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2401 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2401 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2461 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2461 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2521 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2581 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2581 |||||||||||||||||||||||||||||||||||||||||||||||||||||
         GGCCTGCTCACTGTTCCCCATGGGCCCCAGCCAGCCAAGGAACACAGACACTGGACAAG 2640
Db  2641 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CTTCGGCAGGCCGTGACAGAGCTTGTCAGAGTGCGGGAAGGACTGCAGGGGAAGACTGCGCAG 2700

Qy  2641 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CTTCGGCAGGCCGTGACAGAGCTGTCAGAGAGCGTGCGCAGATGCGGGAAGGACTGCGCAG 2700
Db  2701 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         TCACTTCGCCAGGCCTGTGCAGCTTGTCTCTGGCGCCCCACAGGGAGGAGGTCCGTGCCCTCGG 2760

Qy  2701 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2761 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2761 |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2821 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2881 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2941 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GCGTCTCAGAGGGCTCCCCTGGCTGGGCCCCAGAGACCTGTGAGCCGAGCCTGAGCCTCAGACTCA 3000
Db  3001 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3001 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3061 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3121 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  3181 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  3241 ACAGGGGTCTGA 3252
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XX
SQ   Sequence 3857 BP; 677 A; 1301 C; 1201 G; 678 T; 0 other;

  Query Match   99.0%; Score 3218; DB 20; Length 3857;
  Best Local Similarity   99.8%; Pred. No. 0;
  Matches 3244; Conservative   0; Mismatches   5; Indels   3; Gaps   2;

Qy   1 ATGCCGGCCATGCGGGGCCTCCTGGCGCCTCAGAACACCTTCCTGGACACCATCGCTACG 60
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Db   666 GGCCCCGACAGATGGAAAGAGACAGGTGGTGGCCGGCGCCGATATGGCCGGGCACGATCC 725

Qy   481 AAAGGCTTCAATGCCAACCGGCGGCGGAGCCGGGCCGTGCTCTACCACCTGTCCGGGCAC 540
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Db   846 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT 905

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Qy   901 CACTACGTCACCACCTGGTTCCTGCTGGATGTCATCGCAGCGCTGCCCTTTGACCTGCTA 960
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Db   1146 CACTACGTCACCACCTGGTTCCTGCTGGATGTCATCGCAGCGCTGCCCTTTGACCTGCTA 1205

Qy   961 CATGCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCGCCTGCTG 1020
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Qy   1021 CGCCTGCTGCGCCTGCTTCCGCGGCTGGACCGGTACTCGCAGTACAGCGCCGTGGTGCTG 1080
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Db   1266 CGCCTGCTGCGCCTGCTTCCGCGGCTGGACCGGTACTCGCAGTACAGCGCCGTGGTGCTG 1325

Qy   1081 ACACTGCTCATGGCCGTGTTCGCCCTGCTCGCGCACTGGGTCGCCTGCGTCTGGTTTTAC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1326 ACACTGCTCATGGCCGTGTTCGCCCTGCTCGCGCACTGGGTCGCCTGCGTCTGGTTTTAC 1385

Qy   1141 ATTGGCCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1386 ATTGGCCAGCGGGAGATCGAGAGCAGCGAATCCGAGCTGCCTGAGATTGGCTGGCTGCAG 1445

Qy   1201 GAGCTGGCCCGCCGACTGGAGACTCCCTACTACCTGGTGGGCCGGAGGCCAGCTGGAGGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1446 GAGCTGGCCCGCCGACTGGAGACTCCCTACTACCTGGTGGGCCGGAGGCCAGCTGGAGGG 1505

Qy   1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACGGGACGGGGCTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1506 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACGGGACGGGGCTG 1565

Qy   1321 GAGCTGCTGGGCGGCCCGTCGCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1566 GAGCTGCTGGGCGGCCCGTCGCTGCGCAGCGCCTACATCACCTCCCTCTACTTCGCACTC 1625

Qy   1381 AGCAGCCTCACCAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGGACACCGAGAAGATC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1626 AGCAGCCTCACCAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGGACACCGAGAAGATC 1685

Qy   1441 TTCTCCATCTGCACCATGCTCATCGGCGCCCTGATGCACGCGGTGGTGTTTGGGAACGTG 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1686 TTCTCCATCTGCACCATGCTCATCGGCGCCCTGATGCACGCGGTGGTGTTTGGGAACGTG 1745

Qy   1501 ACGGCCATCATCCAGCGCATGTACGCCCGCCGCTTTCTGTACCACAGCCGCACGCGCGAC 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1746 ACGGCCATCATCCAGCGCATGTACGCCCGCCGCTTTCTGTACCACAGCCGCACGCGCGAC 1805

Qy   1561 CTGCGCGACTACATCCGCATCCACCGTATCCCCAAGCCCCTCAAGCAGCGCATGCTGGAG 1620
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1806 CAGCGCGACTACATCCGCATCCACCGTATCCCCAAGCCCCTCAAGCAGCGCATGCTGGAG 1865

Qy   1621 TACTTCCAGGCCACCTGGGCGGTGAACAATGGCATCGACACCACCGAGCTGCTGCAGAGC 1680
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Db   1866 TACTTCCAGGCCACCTGGGCGGTGAACAATGGCATCGACACCACCGAGCTGCTGCAGAGC 1925

Qy   1681 CTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCCTGCAGCTG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1926 CTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCCTGCAGCTG 1985

Qy   1741 CCACTGTTTGAGGCGGCCAGCCGCGGCTGCCTGCGGGCACTGTCTCTGGCCCTGCGGCCC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1986 CCACTGTTTGAGGCGGCCAGCCGCGGCTGCCTGCGGGCACTGTCTCTGGCCCTGCGGCCC 2045

Qy   1801 GCCTTCTGCACGCCGGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCCCTCTAC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2046 GCCTTCTGCACGCCGGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAGGCCCTCTAC 2105

Qy   1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGCTCGCCATCCTAGGG 1920
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Db   2106 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCACCGTGCTCGCCATCCTAGGG 2165

Qy   1921 AAGGGCGACCTGATCGGCTGTGAGCTGCCCCGGCGGGAGCAGGTGGTAAAGGCCAATGCC 1980
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Db   2166 AAGGGCGACCTGATCGGCTGTGAGCTGCCCCGGCGGGAGCAGGTGGTAAAGGCCAATGCC 2225

Qy   1981 GACGTGAAGGGGCTGACGTACTGCGTCCTGCAGTGTCTGCAGCTGGCTGGCCTGCACGAC 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2226 GACGTGAAGGGGCTGACGTACTGCGTCCTGCAGTGTCTGCAGCTGGCTGGCCTGCACGAC 2285

Qy   2041 AGCCTTGCGCTGTACCCCGAGTTTGCCCCGCGCTTCAGTCGTGGCCTCCGAGGGGAGCTC 2100
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Db   2286 AGCCTTGCGCTGTACCCCGAGTTTGCCCCGCGCTTCAGTCGTGGCCTCCGAGGGGAGCTC 2345
```

Qy   3181 GAGATGTGCTATTGGCTGCCATGGCTCTCGGACAGTCCAGTGACCAGGAGAAAGGC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3426 GAGATGTGCTATTGGCTGCCATGGCTCTCGGACAGTCCAGTGACCAGGAGAAAGGC 3485

Qy   3241 ACAGGGTCTGA 3252
          |||||||||||
Db   3486 ACAGGGTCTGA 3497
```

Monkey potassium channel molecule ERG-LP1 cDNA.

```
RESULT 6
AA250452
ID   AA250452 standard; cDNA; 3355 BP.
XX
AC   AA250452;
XX
DT   18-MAY-2000  (first entry)
XX
DE   Monkey potassium channel molecule ERG-LP1 cDNA.
XX
KW   Monkey; potassium channel molecule; ERG-like protein 1; ERG-LP1;
KW   neuroprotective; antiParkinsonian; anticonvulsant; antidepressant;
KW   neuroleptic; nootropic; treatment; CNS disorder; central nervous system;
KW   potassium channel mediated disorder; epilepsy; Alzheimer's disease;
KW   Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia; ss.
XX
OS   Primates.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..103
FT                   /tag= a
FT   CDS             104..3355
FT                   /tag= b
FT                   /product= "ERG-LP1"
FT                   /note= "This region is specifically claimed"
XX
PN   WO200005346-A1.
XX
PD   03-FEB-2000.
XX
PF   21-JUL-1999;  99WO-US-6752.
XX
PR   21-JUL-1998;  98US-0119855.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Curtis RAJ;
XX
DR   WPI; 2000-182682/16.
DR   P-PSDB; AAY44904.
XX
PT   Novel gene encoding potassium channel molecule useful in treating
PT   central nervous system disorders such as Alzheimer's disease, multiple
PT   sclerosis, and schizophrenia
XX
PS   Claim 2; Fig 1; 144pp; English.
XX
CC   The present sequence is a cDNA encoding ERG-like protein 1 (ERG-LP1)
CC   which is a member of ERG potassium channel family. This sequence is
CC   from a full length clone jlkba25d10 which was derived from monkey
CC   hippocampal library. ERG-LP1 is expressed exclusively in the brain.
CC   Highest expression is found in cortical regions, hippocampus, caudate
CC   and amygdala. The protein functions as a potassium channel modulator and
CC   has neuroprotective, antiParkinsonian, anticonvulsant, antidepressant,
CC   neuroleptic and nootropic activities. The present sequence is
CC   useful for treating several potassium channel mediated disorders (CNS
CC   disorders) such as Alzheimer's disease, Parkinson's disease, multiple
CC   sclerosis, epilepsy, depression, schizophrenic disorders and amnesia.
XX
SQ   Sequence 3355 BP; 580 A; 1128 C; 1041 G; 606 T; 0 other;

Query Match             97.0%;  Score 3156;  DB 21;  Length 3355;
Best Local Similarity   98.2%;  Pred. No. 0;
Matches 3192;  Conservative 0;  Mismatches 60;  Indels 0;  Gaps 0;
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```
Qy   2101 AGCTACAACCTGGGTGCTGGGGGAGGCTCTCGCAGAGGTGGACACCAGTCCCTGAGCGGC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2346 AGCTACAACCTGGGTGCTGGGGGAGGCTCTCGCAGAGGTGGACACCAGTCCCTGAGCGGC 2405

Qy   2161 GACAATACCCTTATGTCCACGCTGGAGGAGGAGCAGATGGGGACGCAGGGCCCCACG 2220
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   2406 GACAATACCCTTATGTCCACGCTGGAGGAGGAGCAGATGGGGACGCAGGGCCCCACG 2455

Qy   2221 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCTGTCCCTGGCTCCACCTCC 2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2466 GTCTCCCCAGCCCCAGCTGATGAGCCCTCCAGCCCCTGTCCCTGGCTGCACCTCC 2525

Qy   2281 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGCAGCTCGTCTCAGT 2340
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2526 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGCAGCACCCGCTCGTCTAGG 2585

Qy   2341 GGCAGAGGAGGCCAGGCAGGGCAGGGGCTTTGAAGGCGAGGCTGAGGCTGGCCCCTGCTCCCC 2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2586 GGCAGAGGAGGCCAGGCAGGGCAGGGGCTTTGAAGGCGAGGCTGAGGCTGGCCCCTGCTCC 2645

Qy   2401 CCACGGGCCCTAGAGGGGGCTACGGCTGCCCCCATGGCAATGTGCCCCAGATCTG 2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2646 CCACGGGCCCCAGAGGGCTACGGCTGCCCCCATGGCAATGTGCCCCAGATCTG 2705

Qy   2461 AGCCCCAGGGTAG-AGATGGCATTGAAGACGGCTCGTGGCTCGGACCAGCCCAAGTTCTCT 2520
          ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db   2706 AGCCCCAGGGTAGTAGTAGATGGCATTGAAGACGGCTCGTGGCTCGGACCAGCCCAAGTCTCT 2765

Qy   2521 TTCCGGTGGGCCAGTCCTGCAGTGTACGCAGCAGCCCCCTGGACCAGAGAGC 2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2766 TTCCGGTGGGCCAGTGCTGACAGAGCTGTCAGACGAGTGCTGCAGATGCGGAAGACTGCAG 2825

Qy   2581 GGCCTGCTCACTGTTCCCCATGGGCCCAGCGAGGCAAGGAACACAGACACTGGACAAG 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2826 GGCCTGCTCACTGTTCCCCATGGGCCCAGCGAGGCAAGGAACACAGACACTGGACAAG 2885

Qy   2641 CTTCGGCAGCCGGTGACAGAGCGTGTCAGAGGAAGGACTGCAG 2700
          |||||||||||||||||||||||||||||||||||||||||||
Db   2886 CTTCGGCAGCCGGTGACAGAGCGTGTCAGAGGAAGGACTGCAG 2945

Qy   2701 TCACTTCGGCAGCCTGTGCAGCTTGTCTGTCCTGGCGGCCCACAGGAGGGTCGTGCCCTCGG 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2946 TCACTTCGGCAGCCTGTGCAGCTTGTCTGTCCTGGCGGCCCACAGGAGGGTCGTGCCCTCGG 3005

Qy   2761 GCATCGGGAGAGGGCCGTGCCCAGCCAGCACCTCGGCTTCTGCAGCCTCTGTGTG 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3006 GCATCGGGAGAGGGCCGTGCCCAGCCAGCACCTCGGCTTCTGCAGCCTCTGTGTG 3065

Qy   2821 GACACCTGGGGCATCCCCTACTGCCTGCAGCCCCACCTGGCTCTCGAGTGGGGACT 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3066 GACACCTGGGGCATCCCTACTGCCTGCAGCCCCAGCTGGCTCTGTCTTGAGTGGGGACT 3125

Qy   2881 TGGCCCCACCCGTCCGGGGCTCCGGGGCTCCTCCCCTCCCCATGGCACCCTGGGGTCCCCCA 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3126 TGGCCCCACCCGTCCGGGGCTCCGGGGCTCCTCCCCTCCCCATGGCACCCTGGGGTCCCCCA 3185

Qy   2941 GCGTCTCAGAGCTCCCCCTGGCCTGCTCGAGCCTTCTCACCTCAGACTCA 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3186 GCGTCTCAGAGCTCCCCCTGGCCTGCTCGAGCCCCAGCTTTCTCACCTCAGACTCA 3245

Qy   3001 GAGCCCCTGCCTCTGCTCTAGGAGACCTCTGCTTCTGAGCCACCCGCTCCCCTCCT 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3246 GAGCCCCTGCCTCTGCTCTAGGAGACCTCTGCTTCTGAGCCACCCGCTCCCCTCCT 3305

Qy   3061 TCTGAGGAAGGGGCTAGGACTGGCCCGCAGAGCCTGTCAGACCAGGCTGAGGGCTACCAGC 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3306 TCTGAGGAAGGGGCTAGGACTGGGCCCCGCAGAGCCTGTGAGCCAGGCTGAGGGCTACCAGC 3355

Qy   3121 ACTGGAGAGCAGCCCCCACCAGGGTCAGGGGGCTCAGGGCCTTGGGCCTTGGGCCTCGGACCCCCAGAGCCTG 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3366 ACTGGAGAGCAGCCCCCACCAGGGTCAGGGGGCCTTGGGCCTTGGGCCTCGGGACCCCCAGAGCCTG 3425
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Left column:

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Qy      1 ATGCCGGCCATGCGGGGGCTCCTGGCGGCCTTCAGACACCTTCCTGGACACCATCGCTACC   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    104 ATGCCGGCCATGCGGGGGCCTCCTGGCGGCCTTCGCTTTGCGCTGCCACCATCGCTACG  163

Qy     61 CGCTTCGACGGCACGCACAGTAACTTCG?GCTGGGCAACGCGCCAGGTGGCGGGCGTCTTC  120
          ||||||||||||||||||| |||||||| |||||||| ||||||||||||||||||||||
Db    164 CGCTTCGACGGCACGCACGGCTAACTTCGTGTGGGGCAACGCGCCAGGTGGCGGGCGTCTC  223

Qy    121 CCCGTGGTCTACTGCTTCTCTGTTGACCTTCAGGGGCTTCTCCGGGCTGAGGTC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    224 CCCGTGGTCTACTGCTTCTCTGTTGACCTTCACGGGCTTCTCCGGGCTGAGGTC  283

Qy    181 ATGCAGCGGGGCTGTGCCTGCCTGCTCCTTCCTTATGGGGCCAGACACCAGTAGCTCCTCGC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    284 ATGCAGCGGGGCTGTGCCTGCCTGCTCCTTCCTTATGGGCCAGACACCAGTAGCTCGGCAC  343

Qy    241 CAACAGATACCGCAAGGCCCTGAGCAGAGGAGTTCAAGGCACAGACAGTTCAAGGCTGATAC  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    344 CAACAGATACCGCAAGGCCCTGGACGCACCAAGGAGTTCAAGGCTGATAC  403

Qy    301 CGGAAGAGCGGGCTCCGTTCTGGTTGTCTCCTGGATGTGATCACCCATAAAGAATGAGAAA  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    404 CGGAAGAGCGGGCTCCGTTCTGGTTGTCTCCTGGATGTGATCACCCATAAAGAATGAGAAA  453

Qy    361 GGGGAGGTGGCTCTCTTCCTAGTCTCTCACAAGGCAATCAGCGAAACCAAGAACCGAGGG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    464 GGGGAGGTGGCTCTCTTCCTAGTCTCTCACAAGGCAATCAGCGAAACCAAGAACCGAGGG  523

Qy    421 GGCCCCGACGAGATGGAAGGAGACAGTGGTGGCGGCCGATATGGCCGGGCACGATCC  480
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Db    524 GGCCCCTGACGAGATGGAAGGAGACAGTAGTGGCGGCCGATATGGCCGGGCACGATCC  583

Qy    481 AAAGGCTTCAATGCCAGCCAAGCGGCGGCGGAGCCGGGAGCCGTGCCTCTACCACCTGTCCGGGCAC  540
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Db    584 AAAGGCTTCAATGCCAGCCAAGCGGCGGCGGAGCCGGGAGCCGTGCCTCTACCACCTGTCCGGGCAC  643

Qy    541 CTGCAGAAGCAGCCCAAGGCAGCCAAGCACAAGTCAATAAGGGGTGTTGGGGAGAAACCA  600
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Db    644 CTGCAGAAGCAGCCCAAGGCAGCCAAGCACAAGTCAATAAGGGGTGTTGGGGAGAAGCCA  703

Qy    601 AACTTGCCTGAGTACAAAGTAGCCGGCCATCCGGAAGTCGCCCTTCATCCGTTGCACTGT  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    704 AACTTGCCTGAGTACAAAGTAGCCGGCCATCCGGAAGTCGCCCTTCATCCGTTGCACTGT  763

Qy    661 GGGCACTGAGAGCCACCTCGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCCGTC  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 GGGCGGC?GAGGGCCACCTGGGATGGCTTCATCCTGC?CGCCACGCTCTATGTGGCTGTC  823

Qy    721 ACTGCCCTCACACGTGGTGTGAGCACAGCACGAGCACGGGAGCCCCAGTGCCCGGCGGCCCG  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    824 ACCGTGCTCACCACGTGGTGTGAGCACAGCACGGGAGCCCCAGTGCCCGGCGGCCCA  883

Qy    781 CCCAGCGTCTGTGAACCTGGCCGTGGAGTCCTTCATCCTTGACATTGTGCTGAATTTC  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    884 CCCAGCGTCTGTGAACCTGGCCGTGGAGTCCTTCATCCTTGACATTGTGCTGAATTTC  943

Qy    841 CGTACCACATTCGTGTCCAAGTCGGGCGAGTCGGTGGTTTGCCCCAAAGTCCATTTGCCGG  900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    944 CGTACCACATTCGTGTCCAAGTCGGGCGAGTCGGTGGTGTTCCCCAAAGTCCATTTGCCTC 1003

Qy    901 CACTACGTCACCACCTGGTTCCTGGATGTCATCGGGATGTCATCGGAGTCATCGCAGCCTGCTG  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1004 CACTACGTCACCACCTGGTTCCTGGATGTCATCGGGATGTCATCGGAGCTGCAGCCGTGCTG 1063

Qy    961 CATGCCTTCAAGGTCAACGTACTTCGGGGCCATCTGCTGAAGACGCGTGCCCTGCTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1064 CATGCCTTCAAGGTCAACGTACTTCGGGGCCTCTACCCGCTGAAGACGCGTGCCCTGCTG 1123

Qy   1021 CGCCTGCTGCGCCTTCCCGGGCTGGACCCGGGACTACTTCGCAGTACGCGCCGTGGTCTG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1124 CGCCTGCTGCGCCTTCCCGGGCTGGACCCGGGACTACTTCGCAGTACGCGCCGTGGTCTG 1183
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Right column:

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Qy   1081 ACACTGCTCATGCCGCTGTTCGCCCTGCTCTCGCGCACTGGCTCGCCGTCGCTCGGTTTAC 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1184 ACACTGCTCATGGCGCCTGTTGCCCTGCTTGCGCCGCTGGCTGGCTGGCTGCTCTGGTTTAC 1243

Qy   1141 ATTGGCCAGCGGGAGATCGAGAGCGCGCAGCGGGAATCCAGCTGCCTGCCTGAGATTGGCTGGCTGCAG 1200
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Db   1244 ATTGGTCAGCGGGAGATCGAGAGCAACGGGCAGCACCGAGTCCAGCTGCCTGAGATTGGCTGGCTGCCAG 1303

Qy   1201 GAGCTGCCGCCGCCACTGGAGACTCCCTACTACCTGGTGGGCCGGAGGCCAGCTGGAGGG 1260
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Qy   1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCGGCGGCGGGACGGGGGCTG 1320
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Db   1364 AACAGCTCTGGCCAGAGTGACAACTGCAGCAGCAGCAACGGGACGGGGGCTG 1423

Qy   1321 GAGCTGCTGGGGCGGCCCTGCGCCAGCGGCTCACGCCCTACACTTCACCTTCCCACTC 1380
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Db   1424 GAGCTGCTAGGCGGGGGCCCGTCGCGGCCAGGGCTACATCACCTCACTTCACTCGCACTC 1483

Qy   1381 AGCAGCCTCACCAGCTGGGGCTCGGCGGGCAACGTGTCCGCCAACACGGACACCGAGAAGATC 1440
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Db   1484 AGCAGCCTCACCAGCTGGGGCTTCGGCAACGTGTCCGCCAACACGGACACTGAGAAGATC 1543

Qy   1441 TTCTCCATCTGCACCATGCTCACCGGCGTGACGCGGCCTGGTGTTTGGGGAACGTG 1500
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Db   1544 TTCTCCATCTGCACCATGCTCACCGGCGGGTGGTGTGTCGGGGAACGTG 1603

Qy   1501 ACGGCCATCATCCAGCGGCATGTACGCGCCCGCCGCCCGCTTTCTGTACCACAGCCGCCGGAC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1604 ACGGCCATCATCCAGCGGCATGTACGCGCCGCCCGCTTTCTGTACCACCAGCCGCCGGAC 1663

Qy   1561 CTGCGGACTACATCCCGATCACCGTATCCCCAAGCAGCCCCTCAAGCAGCCATGCTGGAG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1664 CTGCGGACTACATCCCGATCACCGTATCCCCAAGCAGCCCTCAAGCAGCCATGTCTGGAG 1723

Qy   1621 TACTTCCAGGCCCACCTGGGCGGTGAACAATGCCATCGGCGCTGGGCAGGGCTGCGAGAGC 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1724 TACTTCCAGGCCGACCTGGGCGGTGAACAATGGCATCGGCGCTGGGCAGGGCTGCAGAGC 1785

Qy   1681 CTCCCTGACGAGCTGCGCGGCGGCCAGACACTGCACCATGCCATCTGCACGTGCTGCAGCTG 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1784 CTCCCTGACGAGCTGCGCGGCGGCCAGACACTGCACCATGCCATCTGCACTGCTGCAGCTG 1843

Qy   1741 CCACTGTTTGAGGGCGGCACTGCCTGCCTGCGCCGGCGGCCACTGTCTCTCGCCCCTCGCGGCCC 1800
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1844 CCGGTGTTTGAGGAGCGGCAGCGGGCCTGCGCCGGCGGCCACTGTCTCTCGGCCCTGCGGGCCC 1903

Qy   1801 GCCTTCTGCACGCCGGGCGGAGTACGCGGATACCTCACCACCAAGGCATCTCAGGGCCCTCTAC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1904 GCCTTCGCACGCCGGGCGGAGTACGCGGATACCTCATCCGCAGTGCCCTGCAGGGCCCCTAC 1963

Qy   1861 CTCCCTGACGACGTGCTCATGGAGGTGCTTCAAGGTGCACCGGACACCGTGCTTCTCTGCCCTCTAGGG 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1964 CTCCCTGACGAGGTGCTCATGGAGGTGCTTCAAGGTGCACCGGACACCGTGCTTCTCTGCCCATCTAGGG 2023

Qy   1921 AAGGGCGACCTCATCGGCCTGTGAGCCTGCCCCGGCGGAGCCAGGTGGTAAAGGCCAATGCC 1980
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2024 AAGGGTGACCTGATCGGCCTGTGAGCCTGCCCCGGCGGAGCCAGGTGGTGAAAGGCCAACGCC 2083

Qy   1981 GACGTGAAGGGGCTGACGTACTGCGTCTGCACCTGCGGCCTGCACGAC 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2084 GATGTGAAGGGGCTGACGTACTGCGTCTGCGACAGTGTCTGCACGAC 2143

Qy   2041 AGCCTTGCGCTGTACCCCGAGTTGCCCCGCGCTTCAGTCGTGCGCTCCGAGGGGAGCTC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2144 AGCCTTGCGCTCTACCCCGAGTTTGCCCCGCGCTTCAGCCGTCGCTCCGAGGGGAGCTC 2203

Qy   2101 AGCTACAACCTGGGTCTGCTGGGGGAGGCTCTGACGAGAGGTGGACACCAGCGCCTCCTGAGCGGC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2204 AGCTACAACCTGGGTGCTCCGGGGGAGGCTCTGAGAGGTGGACACCAGCGCCTCCTGAGCGGGC 2253

Qy   2161 GACAATACCCTTATGTCCACGTGGAGGAGGAACAGATGGGAGCAGGGCCCACG 2220
```

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Db    3344 ACAGGGGTCTGA 3355

RESULT 7
AAX84919
ID   AAX84919 standard; DNA; 3715 BP.
XX
AC   AAX84919;
XX
DT   28-SEP-1999  (first entry)
XX
DE   Rat brain specific potassium channel protein coding sequence.
XX
KW   Brain specific potassium channel; central nervous system disorder;
KW   dementia; cerebral ischaemic sclerosis; therapy; probe; ss.
XX
OS   Rattus sp.
XX
PN   WO9937677-A1.
XX
PD   29-JUL-1999.
XX
PF   20-JAN-1999;  99WO-JP00190.
XX
PR   04-DEC-1998;  98JP-0346198.
PR   23-JAN-1998;  98JP-0011434.
XX
PA   (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
PI   Miyake A,  Mochizuki S,  Yokoi H;
XX
DR   WPI; 1999-458683/38.
XX
PT   Potassium channel protein expressed specifically in brain tissue and
PT   method for its production
XX
PS   Example 3; Page 54-57; 63pp; English.
XX
CC   This sequence encodes a rat potassium channel protein, and was used as a
CC   probe to isolate DNA encoding the protein of the invention. The protein
CC   of the invention is a human brain specific potassium channel protein. The
CC   protein is used to treat and investigate disorders of the central nervous
CC   system such as dementia and cerebral ischaemic sclerosis.
XX
SQ   Sequence 3715 BP; 735 A; 1167 C; 1090 G; 723 T; 0 other;

Query Match             81.9%;  Score 2664.8;  DB 20;  Length 3715;
Best Local Similarity   89.0%;        Pred. No. 0;
Matches 2905;  Conservative   0;  Mismatches 347;  Indels  12;  Gaps  2;
```

```
Qy      1 ATGGCGGCCATGCGGGCCTCGGCCCTCCTGGACACCACCATCGGCTACG  60
          ||||||||||||||||||||||||| |||||||||||||||| |||||||
Db    156 ATGCGCGGCCATGCGGGGGCTCCTGGCCGCCGCAGAACACCTTCCTGGACACCACCATCGGCCACC  215

Qy     61 CGCTTCGACGGCAGCAGGCACGCACGTAACTTCGTGCGTGGGCCAAGCGCCAGGTGGCGGGGCTCTTC  120
          |||||||||||||||| ||||||||||||| ||||||||||||||||||||||||
Db    216 CGCTTCGACGGGGAGCGGGACGCACAGTAACTTCGTGCGTCTGGGGCAACGGCCAGGTGGCAGGGCTCTTC  275

Qy    121 CCCGGTGGTCTACTGCGTCTGATGGCTTCTCCGGGCTGAGGTC  180
          | |||||||||||| |||||||||||||||||||||| ||||||||
Db    276 CCTGTGGTCTACTGCTCCGATGGCTTCTCCGATGGCTGAGGTC  335

Qy    181 ATGCAGCGGGGCCTGTGCCTGCTCCTTTATGGGCCAGACCAGTGAGCTCGTCCGC  240
          ||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db    336 ATGCAGCGAGGCGTGTGCCTGCTCCTTCCTCTATGGGCCAGACCACCAGTGAGTTGGTCCGC  395

Qy    241 CAACAGATCCGCAAGGCCTGGCGCAGCAGCGACACAAGAGGC  300
          ||||||||||||||||||||||||||||||||| ||||||||
Db    396 CAACAGATCCGAAAAGCCCTGGATGAGCACAAAGAATTCAAGGCTGAACTGACTGATCCGTAC  455

Qy    301 CGGAAGAGCGGGCTCCGTTCTGGTCTCTCCGGATGTGATACCCATAAAGATGAGAAA  360
          ||||||| ||||| |||| |||||
Db    456 CGGAAGAGCGGGCTTCCATTCGGTGTCTCGGATGTGATACCTATAAAAAACGAGAAG  515
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Sequence alignment continuation (right column):

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Db    2264 GACAATACCCTTATGTCCACGTCCAGGGAGCAGATGGGGAGCAGGCCCCCACA  2323
Qy    2221 GTCTCCCCAGCCCAGCTGATGAGCCCTCCAGCCCTCGTGTCCCCGTGGCTGCCACCTCC  2280
Db    2324 GTCTCCCCAGCCCAGCTGATGAGCCCTCCACTGCCCCTGGTTGCCACCTCC  2383
Qy    2281 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTGAACAGCACCCGGCTCGTCGTCTAGGT  2340
Db    2384 TCATCCTCGGCTGCCAAGCTGCTATCCCCACGTCGAACAGCACCCGGCTCGTCGTCTAGGT  2443
Qy    2341 GGCAGGAGGAGGCAGGCAGGCAGGGCTTTGAAGGCTGAGGCTGGCCCCTCGTGCTCCC  2400
Db    2444 GGCAGGAGGAGACCAGGCAGGCAGGGCTTTGAAGGCTGAGGCTGGCCCCTCTGCTCCC  2503
Qy    2401 CCACGGCCCTAGAGGGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCCAGATCTG  2460
Db    2504 CCACGGGCCCTAGAGGGGGCTACGGCTGCCCCCATGCCATGGAATGTGCCCCCAGATCTG  2563
Qy    2461 AGCCCCAGGTAGTAGTGATAGCGGCATTGAAGACGGCTGTGCCTCGGACCCCAAGTTCTCT  2520
Db    2564 AGCCCCAGGTAGTAGTGATAGCGGCATTGAAGACGGCTGTGCCTCGGACCCCAAGTTCTCT  2623
Qy    2521 TTCCCGTGGGCCAGTCGGCCTGGCCCGGAATGTAGCAGCAGCCCCCTCCGGAAGAGAGC  2580
Db    2624 TTCCCGCATGGGCCAGTCGGCCTGGCCCGGAATGTAGCAGCAGCCCCCTCCGGAAGAGAGT  2683
Qy    2581 GGCCTGCTCACTGTCCCCATGGGCCCAGCGAGGCAAGGACACAGAACACTGGACAAG  2640
Db    2684 GGCCTGCTCACTGTCCCCCATGGGCCCAGCGAGGCAAGGACACAGAACACTGGACAAG  2743
Qy    2641 CTTCGGCAGCCGGTGACCAGACGTGTCAGAGACAGGTGCTGCAGATGCGGGAAGGACTGCAG  2700
Db    2744 CTTCGGCAGCCGGTGATGGAGCTGCAGAACAGTGCTGCAGATGCGGGAAGGACTACAG  2803
Qy    2701 TCACTTCGGCCAGGCGTGTGCAGCGTTGTCCTGGCCCCCACAGGAGGGTCCGTGCCTCGG  2760
Db    2804 TCACTTCGGCCAGGCGTGTGCAGCGTTGTCCTGGCACCCCATGCCGTCCGG  2863
Qy    2761 GCCATCGGAGAGGGGCGCTGCCCAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTG  2820
Db    2864 GCCTCAGGAGAGGGGCCATGCCAGCGAGCCAGCACCTCCGGGCTTCTGCAGCCTCTGTGTG  2923
Qy    2821 GACACTGGGCATCTCCTACTGCCTGCAGCCCCCAGCTGGCTCTGTCTGTGTGGGGACT  2880
Db    2924 GACACTGGGGCATCCTCCTACTGCCTGCAGCCCCCAGCTGGCTCTGTCTGTGAGTGGGGACT  2983
Qy    2881 TGGGCCCCACCCGTCCGCCGGGGCTCCTCGTCGTCCTCCATGGCCGTGGGGTCCCCA  2940
Db    2984 TGGGCCCCACCCGTCCGGGGGCTCCTCGTCTGGCGTCCATGGCCGTGGGGTCCCCCA  3043
Qy    2941 GCGTCTCAGAGCTCCCCGGCCTCGAGCCACAGCTTCTGGACCTCAGACTCA  3000
Db    3044 GCATCTCAGAGCTCCCCGGCCTCGAGCCACAGCTTCTGGACCTCAGACTCA  3103
Qy    3001 GAGCCCCTGCCTCAGGAGAGACCTCTGTCTGAGCCCAGCCACCCCTGCCCCTCCTCCT  3060
Db    3104 GAGCCCCTGCCTCGACGGAGACCTGCTGCCTGAGGCCCAGCCACCTCCT  3163
Qy    3061 TCTGAGGAAGGGGCTACGGACTGGGCCCGCCAGCCTGAGGCTGAGGCTACCAGC  3120
Db    3164 TCTGAGGAAGGGGCTACGGACTGGGCCCCCCAGCTGTTGAGGCTGAGGCTACCAGC  3223
Qy    3121 ACTGGGAGAGCCCCACCAGGGGTCAGGGGGCCGTCAGGGGCCTTGCCTGGACCCCAGCCTG  3180
Db    3224 ACTGGGAGAGCCCCGCCCCCGCCAGTGTCAGGGGGCCTTGCCTGGACCCCAGCCTG  3283
Qy    3181 GAGATGGTGCTTATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGC  3240
Db    3284 GAGATGTGCTTATTGGCTGCCACGGCTCTGGCACAGTCCAGTGGACCCAGGAAGAGGC  3343
Qy    3241 ACAGGGGTCTGA 3252
          ||||||||||||
Db    3344 ACAGGGGTCTGA 3355
```

Qy 1432 GAGAAGATCTTCTCCATCTGCACCATGCTCATCGGCGCCCGATGCACGCGGTGGTGTTT 1491
         ||||||| |||||||||| |||||| |||| ||||||||||||||| | ||||||||||
Db 1596 GAGAAGATTTCTCCATCTGCACCATCTGCTATTGGAGCTCTGATGCAGTGGTGGTGTT 1655

Qy 1492 GGGAACGTGACGGCCATCATCCAGCGCCCGCG TTCTGTACCACCAGCCGC 1551
         ||||||| ||||||||||||||||||||||| | ||||| ||||||||||
Db 1656 GGGAATGTGACAGCCATCATCCAGCGCCATGTACGCGCCGCTTCTGTACCAGCAGCCGC 1715

Qy 1552 ACGGCGACTGCGGCACTACATCCACCGTATCCGCATCCCCTCAAGCAGCGAC 1611
         || || ||||||||| ||||||||||||||||||||||||||||||||||||
Db 1716 ACCCGTGACCTGGAGACTACATTCGCATCCACCGCATCCCCAAGCAGCGGC 1775

Qy 1612 ATGCTGGAGTACTTCCAGGCACCTGGGCGTGAACAATGCATCGACCACCGAGCTG 1671
         || ||||||||| |||||||||||||| |||| ||||||||||||||||||||||
Db 1776 ATGCTCGAGTACTTCCAAGCACCTGGGCCGTGACAACGGCATCGACACTGAGCTG 1835

Qy 1672 CTGCAGAGCCTCCCTGACAGCTGCGGCGACAGCTGCCATCGCAGAGGAGGTC 1731
         || ||||||||||| | || |||| |||||||||||||| |||||||||||||
Db 1836 CTGCAGAGCCTCCTCCGGATGAGCTTCGAGCAGCAGCACATCGCCATCGCACAAGGAGGTC 1895

Qy 1732 CTGCAGCTGCCACTGTTTGAGGCGGCAGCCGGCTGCCTGGGCCACTGTCTTTGGCC 1791
         |||||||| |||| |||||||||| |||||| ||||||||||||||||||
Db 1896 CTGCAGCTGCCATTGTTCGAGGCAGCAGCCGGCTGCCTGCGGCCACTGTCTCTGGCC 1955

Qy 1792 CTGCGGCGCCGCCTTCTGCACGCGCCGGGCCGGAGTACCTCATCCACCAAGGCGATGCCCTGCAG 1851
         || |||||||||||||| |||| |||||||||||||||||||||| ||||||||| ||||||||
Db 1956 CTGAGGCGCCGCCTTCTGCACGCGCCGGGCCGAGTACCTCATTCACCAAGGCGATGCTCTTCCAG 2015

Qy 1852 GCCCTCTACTTGTCTGCTCGGAGGTCCTCATCGGTTCAAGGTCGGCACCGTCTCGCC 1911
         |||||||||||| |||| |||||||||||| |||||| ||||||| ||||||||||||
Db 2016 GCTCTCTACTTTGTGTGCTCAGGTTCCATCGGAGGTCCTCAAAGGTGGCACCGTCTCGCC 2075

Qy 1912 ATCCTAGGGAAGGGCGACCTGATCGGCTGTGAGCTGCCCCGGCGAGCAGTGGTAAAG 1971
         || |||||||||||||||||||||| ||||||||| || |||| || ||||||| |||
Db 2076 ATTCTAGGGAAGGGTGACCTGATCGGCTGTGAGCTGCCCCAGCAGCAAGCAAGTAGTGAAG 2135

Qy 1972 GCCAATGCCGACGTGAAGGGCTGAAGGGCTACTGCGGCTGTCTGCAGCTGGCTGGC 2031
         ||||||||||||||| |||||||||||||||||||| |||||||||||||||||||
Db 2136 GCCAATGCCGACGTAAAGGGCTGACATACTGCGTCTGACAGTCGTGCCTGGGCTGGG 2195

Qy 2032 CTGCACGACAGCCTTGCGGAGTTGCGCCGCGTTCAGTCGTTGGCCGCITTCAGTGTCGGCCTCCGA 2091
         ||||||||||||||||| ||||||||||||||| ||||||||||||||||||||||||||| ||
Db 2196 CTGCACAGAGCCCTGCACTGTACCCTGAGTTGCCCACGCGTTGCCCACGGCTTAGCGTGGCCTCCGA 2255

Qy 2092 GGGGAGCTCAGCTACAACCTGGGTGCTGCCAGTACCGCAGCCGTGCTCTCAGAGGTGGA ACCAGCTCC 2151
         |||||||||||| |||||||||| ||||| |||||||||||||||||| || |||| ||||||||||
Db 2256 GGGGAGCTCAGCTACCAACCTGGGAGCTGGGAGTGTCGTCGCAGAGTGGGATACCAGCTCA 2315

Qy 2152 CTGAGCGGCGACAATACCCTTATGTCCACGCTGGAGGAGGAGAGAGACAGATCGGGAGCAG 2211
         ||| ||||||||||||||| ||||||| |||||||||||||| ||||| ||||||||||
Db 2316 CTGAGTGGTGACAACACCCTCATGTCCACAGTGACAACTAGGGGCAGGATGGGGAGCAA 2375

Qy 2212 GGGGAGCTCACGGTCTCCCAGCCCCAGCCCCCACGTGAGTGAGCCCTGCTCGTCCCCTGGC 2271
         ||||||||||||||||||||||||||||||||||||| ||| |||||||||||||||||||||
Db 2376 GGACACACGATCTCACCACGCACAGATGAGCCCTCCAGCCCCTGCTGCTCAACTGGC 2435

Qy 2272 TGCACCTCCTCATCCTCAGCTGCCCAAGCTGCTATCCCACGTGACAACAGCACCCCCGGCCT 2331
         || |||| ||||||||| || | |||||||||||| | |||||| |||||||| ||||||| ||
Db 2436 TGTACCTCCTCCTCTCCTCAGCGGCCCAAATACTCTCCCCCAGTGCACCCCGCCCCCGGCCG 2495

Qy 2332 CGTCTAGGTGGCAGAGGGGCGGGGCCACAGGGCCCAGGCAGGGCTTTGAAGGCTGAGCGTGCCCC 2391
         ||||||| |||||| ||||||||||||| |||||||||||||||||||| ||||||||||||||||
Db 2496 AGGCTGGGTGGCAGAGGGGCGGGGCAGGGGTTTGAAGCTGAGGCTGCCT 2555

Qy 2392 TCTGCTCCCCCACGGGCCCCTAGAGGGCTACGGCTGCCCCATGGAATGTGCCC 2451
         ||||||||||||||| |||||||||||| |||||||||||||||||| |||||
Db 2556 TCTGCTCATCCACGACACTGATGGGTTGCAGTCGCCCCCATGCCCCTTGTAC 2615

Qy 2452 CCAGATCTGAGCCCCCAGGGTAGTAGCATTGAAGACGGTCGCCAGACCGTGTGCCTCTGGACCAGCC 2511
         |||| || ||||||||| || || ||| | ||||| ||| |||||||| || || ||||||||||||
Db 2616 CCAGACCTGAGCCCCAGGGTGCTGTAGATGGCGTAGACGGTGCCGGCTCTGACCAGCAC 2675

Qy 2512 AAGTTCTCTTTCCGCGTGGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCCCCTGGA 2571
         ||||||||| ||||| || |||||| ||||||||| |||| || ||||||||||||||
Db 2676 ...

Qy   361 GGGGAGGTGGCTCTCTTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGG 420
Db   516 GGGGAGGTGGCCCTCTCCTGGTCTCTCACAAGGACATCAGTGAGACACAAGACCAGGA 575

Qy   421 GGCCCCGACAGATGGAAGGAGAGCAGGTTGGTGCGGGCCGATATGGCGGGCAGGATCC 480
Db   576 GCCCCTGACAACTGGAAGGAGAGGTCGTGGCGGCCGAGTATGGTCGGGCAGGATCC 635

Qy   481 AAAGGCTTCAATGCCAACCGGCGGCGGGCGGGCCGGGCCCTGCTCTACCACCTGTCCGGGCAC 540
Db   636 AACCGTGACCTGGAGACTACATTCGCATCCACCAAGCCCCAAGCAGCAC 695

Qy   541 CTGCAGAAGCAGCCCAAGGCACAAGCACACAGCTCAATAAGGGGTGTTTGGGGAAAACCA 600
Db   696 CTGCAGAAACAACCCAAGGCACAAGCACAAACTCAATAAGGTGTGTTTGGGGAGAGAAGCCA 755

Qy   601 AACTTGCCTGAGTACAAAGTAGCCCATCCGGAAGTCCCCTTCATCCTGTTGCACTG 660
Db   756 AATTTGCCCGAATATAAAGTCGCTGCTATCCGGAAGTCACCCTTATCCTGCTGCACTGT 815

Qy   661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCGCTCGCCCACACTCTATGTGGCTGTC 720
Db   816 GGGGCTGTGAGAGCCACCTGGGATGGCTTCATCCGCTCGCCCACGCTCTACGTGGCTGTC 875

Qy   721 ACTGTGCCTACAGCGGTGTGTGTGAGCACAGCACGCGGGCCCAGTGCCCCAGCCCCCCCG 780
Db   876 ACTACTGCCATACAGCGGTGTGTGAGCACAGCACGCGGGCCCAGTGCTGCCCCGTGGCCCCA 935

Qy   781 CCCAGGCTCGTGACCTGGCCTGGAGTTCCTTCATCCTTGACATTGTGCTGAATTTC 840
Db   936 CCTAGTGTCTGGACCTGGCCTGGGGCTCCTCACACTTTAGATAIGTGCTGAATTTT 995

Qy   841 CGTACCACCATTCGTGTCCAAGTCGGTGIGTTGCCCCAAAGTCCATTTGCCTC 900
Db   996 CGTACTACATTTGTGTCCAAGTCAGGGCGTATTCGCCCCCAAAGTCCATTTGCCCTC 1055

Qy   901 CACTACTCACCACCTGGTTCCGCTGGATGTCATCGGACGGGCTCCTTGACCTGCTA 960
Db 1056 CACTACGTCACCACCTGGTCCTCGGATGTCAGTCCCACTGCCCTTTGACCTACTA 1115

Qy   961 CATGCCTTCAAGGTCACGTGTTACTTCGGGGCCCATCTGCTGAAGACGGTGCGCCGCTG 1020
Db 1116 CATGCCTTCAAGGTCACGTGTTTGGGGCTCACCACTGCCCTGCTGAAGACGGCGCGGCTG 1175

Qy 1021 CGCCTGCTGCGGCCGCTCTCCGGGCTGCTGACCCGGTACTCGCAGACCGTGTCCTG 1080
Db 1176 CGGCTGCTGCGGCCGCTACTACCAAGACGGACCGGCGACTCTCAGTAIAGCCGTGTCGTC 1235

Qy 1081 ACACTGCCTCATGGCCGTGTTCGCCCGCGTGGTGGTTTAC 1140
Db 1236 ACCTTGCTCATGGCTGTGTTGCCGTGTTGCCCACTGGGTCGTTGGTTCTAC 1295

Qy 1141 ATTGGCCAGCGGGAGATCGAGAGCAGCAGCGAGATTCCAGCTGCCTGAGATTGGCTCGGCTGCAC 1200
Db 1296 ATCGGGCCAGCAGAGATTGAGAACAGCGAGTCAGAGCTGCCTGAGATCGGCTGGCTGCAC 1355

Qy 1201 GAGCTGCCCCGGACTGGAGACTCCCTACTACCGGTGGGGCCCAGCTGGAGGG 1260
Db 1356 GAGCTGCCACGGAGGCTGAGACGCCCTATTACCTGGTGAGCCCAGAGTGCAGATGGAGGG 1415

Qy 1261 AACAGCCCGGCCAGAGTGACAACTGCCAGCAGCA------GCAGCGAGGCGCAACGG 1311
Db 1416 AACAGCGTCTGGCCAGAGTGAAAAACTGCCAGCAGCCAACGG 1475

Qy 1312 ACGGGGCTGCTGGGCGCCCGTGCCTGCTGCCAGCGCCTACATCACCTCCTCTAC 1371
Db 1476 ACTGGGCTGCTGGGCTGGGTGCCCATCCCTACGCAGCCAGCGCCTACATCACCTCCTTGTAC 1535

Qy 1372 TTCGCACTCAGCAGCCTCAGCAGCCTGTGGGCTTCGGCAACGTGTCCCGCAACACGGACACC 2431
Db 1536 TTCGCGGCTCAGCAGTCTCACCCAGTGGGCTTCGGCAATGTGTCGCCGCTAACACAGACACT 1595

```
Db   2676 AAGTTCTCTTTCCGGGTGGGTCAGTCTGCCCGGAGAATGTAGCAGCAGCCCCTCCCCAGGA 2735
          |||||||||| |||| ||||||| ||||||| || ||||||||||||||||||||| ||

Qy   2572 CCAGAGAGCGGGCTGCTCACTGTTCCCATGGCCAGCGAGGCAAGGACACAGCACACA 2631
          ||||||| |||||||||||||| |||||: |||||||||||||||||||||||||||

Db   2736 ACAGAGAGAGTGGCCTGCTCACTGTCCCTTGGTGCCCAGTGAGGCAAGAAACACAGACACA 2795

Qy   2632 CTGGACAAGCTTCGGCAGCGGCGGTGACAGAGCTGTCAGAGCAGGTGCTGCAGATGCGGGAA 2691
          |||||||||||| |||||||||||| || ||||| |||||||||||||||| ||||||||||

Db   2796 CTGGACAAGCTACGGCAGCGCGGTGACGGAGCTGTCTGAACAGGTGCTGCAGATGCCGGAGAG 2855

Qy   2692 GGACTGCAGTCACTTCGCCAGCGTCTGCAGCTTGTCTGGCGCCCCACAGGAGAGGTCCG 2751
          |||||||||||||||||||||||||| |||||| |||||: ||||| |||| | :

Db   2856 GGACTGCAGTCAGTTCGCCAGCGTGTGCAGCTCATCCTGGTGCCCCAAGGGGAAGGCCAG 2915

Qy   2752 TGCCCTCGGGCATCGGGAGGAGGGCCGTGCCCAGCCAGCCACCTCCGGGCTTCTGCAGCCT 2811
          |||||||:|||| |||||||| ||||| ||||| || ||||||||||| |||||||| ||

Db   2916 TGTCCCCGGTATCGAGCAGAGGGCCCTGCCCCGTGCCTCCTCGGGCTCCTACAACCC 2975

Qy   2812 CTGTGTGTGGACACTGGGGCATCCTCTACTGCTGCAGCCCCAGCTGGCTCTGTCTTG 2871
          |||||| ||| ||||||||: ||||| |||||||||||||| || ||| ||||||| ||

Db   2976 CTGCGTGTGGACACTGGGGCATCATCCTACTGCTGCAGCCCCAGCAGTTCAGTCTTG 3035

Qy   2872 AGTGGGACTTGGCCCACCCTCGTCCGGGGCCT---CCTCCCCTCATGGCACCCTGCCC 2928
          ||||||||||||:||||| ||||| ::|||||      |:||||||||||||||||||||

Db   3036 AGTGGGACCTGGCCTCACCCCGTCCAGGGCCATCCCCGTCCAGGGCATGGCACCCTGCCCC 3095

Qy   2929 TGGGGTCCCCCAGCGTCTCAGAGCTCCCCGGCCTCGAGCCACAGC-TTCTGGACCTCC 2988
          |||||||||||||||||||||||||:||||||||||||| ||||| |||||||||||||

Db   3096 TGGGGCCCCCCAGCATCTCAGAGCTCCCCGGCCTCGAGCCCACAGCTTTATGGACC:CC 3155

Qy   2989 ACCTCAGAGACTCAGAGCCCCCTGAGCAGGACCTCTGC TCTGAGCCAGCACCCTGCC 3048
          ||||||||||||||:|||| |||||||| |||| |||| |:||||||||||||||||||

Db   3156 ACCTCAGAGACTCAGAGCCCCTGGCTCTGCTGGAGACCTCTGTGAGCCAGCACCCTGCC 3215

Qy   3049 TCCCTCCTCCTTCTGAGGAAAGGGCGTAGGGACTGGGGCCCCCAGAGGGCCTGTGAGCCAGGCT 3108
          |||||||||| |||||||||||||||| ||||| ||||||: ||||| |||||||||||||

Db   3216 TCACCCCTCCTCCTGAGGAAGAGAGCTAGGAGCTGGGACTCCTGCCACCTGTGAGCCAGGCT 3275

Qy   3109 GAGGCTACCAGCACTGGAGAGCCCCCACCAGGGTCAGGGCCTTGCCTGGAC 3168
          |||||||||||||||||| :|||||||||||||| ||||||||:|||||||||

Db   3276 GAGGCTACCAGTACTGGAGAGCCCCTCACCAGGGTCAGGGCCTCACCGAGGTC 3335

Qy   3169 CCCCACAGCCTGGAGATGTGCTTATTGGCTGCCATGGCCTCTGGCACAGTCCAGTGGACC 3228
          |||||||||||||||||||| ||||| ||| |||||||:||| |||||||||||||||||

Db   3336 CCCCACAGCCTGAGATGGTGCTCATCGGCTGCCATGGCCTCGGCTCCAGTGGACC 3395

Qy   3229 CAGGAAGAGGCACCAGGGGTCTGA 3252
          ||||| || |||||||||||||||

Db   3396 CAGGAGGAGGGCACCAGGAGTCTGA 3419
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Query Match   27.2%; Score 884.8; DB 20; Length 3064;
Best Local Similarity   65.5%; Pred. No. 1.3e-151;
Matches 1408; Conservative   0; Mismatches 622; Indels 120; Gaps   3;

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Qy    1 ATGCCGCCATGCGGGGGCCTCCTGGCGCCTCAGAACACCTTCTGACACCATCGCTACG 60
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Db    4 ATGCCGCGTCATGAAGGGGTGCTGGCCCCGCAAAACACCTTCCTGGACACCATCGCCACC 63

Qy   61 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGCCCAGTGGCCGGGGTCTTC 120
         ||||||||||| ||||||||| ||||| |||||||||||: |:|| |||||||||||

Db   64 CGTTTGACGGCAACGCACAGCTTCCTGCTGGCCAACTTCCTGCTGGCCCAACCCACACGGGGCTTT 123

Qy  121 CCGTGGTCTACTGCCTCTGATGGCTTCTGTGACCTGCAGCATGCAGCCAGCATGAGCTCGAGGTC 180
         |||::|||| |||||||| || :|||:|||||:||: ||||:|| ||||| :||||||||||||||

Db  124 CCCATGTCTACTGCTCCGACGGCGTTCGCGAGCTCAGCATGCGTCGCACCAGGGTCGCACCGAGGTC 183

Qy  181 ATGCAGCGGGGTGTGCCTGCTTATTGGCGTCCTCCTTTATGGGCCAGCACCAGTGAGCTCGTCCGC 240
         ||||||:|| |: ||| ::||||||| |||| | :||||| ||||||||||||||||||| ||||

Db  184 ATGCAGAGAGACCTGCAGCTGCGTTCCGTTTCCTCCTACGGCCCAGACCAGGACCAGCGCCCTG 243

Qy  241 CAACAGATCCGCAAGGCCCTGACGACGAGCACAAGGAGTTCAAGGCTGATCCTGTAC 300
         | ||| || || :|||:||||||||||||||:|| ||| |||| |||:|||||||||

Db  244 CAGCGTCTGCACAAAGCCCTGGAGGCCCACCGAGGCGTGAAAATCTGTTCTCTAC 303

Qy  301 CGGAAGAGCGGGGCTCCGTTCTGGTGTCTCCTGGATGTGATGGACATGAATCAAGAAATGAGAATG 360
         | || |||::|||||| |:|:| ||||| ||||||||||||: |||||||||||||||||||||||

Db  364 CGCAAGGGATGGCGGCTTCAGCGTTTCTGGACATGAATCAAGAGAATCAAGAATGAGATG 363

Qy  361 GGGGAGGTGGCTCTCTTCTCCAGTGTCTCTCCACAAGGACATC-----AGCGAAAGCAAGAAC 414
         |||||| ||:|||:|| ||:|| : || |  ||||| || |||      |  ||||||||||

Db  364 GGGGAGGTCGTGCTGTTCCTTCCTTTCCCTTCAAGGATATCAGTCTTCCTTCAAGGATATCACTGAAGTCGAAGCCCAGGA 423

Qy  415 CGAGGGGCCCCCGACAGATGGGAAAGAGACAGAGCAGTTGTGCCGGCCGATATGGCGCGGGCA 474
         ||| ||| ||| |||:|| : ||| ||| |:|| |||||||:|||||: :||||||||||||

Db  424 CTTGGCCCCCCAAGGAGGGCGGGCGGGGAACGTAATCACGAAAAACTCCTTGGTAGGAGGGGA 483

Qy  475 CGATCCAAAGCTTCAATGCCAACCGACGGGAGCCGGGCCGGCGCTCTTACCACCTGTCC 534
         |: | ||| | :||:|||| |:|| |||||||:||||||| || ||||:|||||| |||

Db  484 GCCACCTGGAAATTTCGGTCGTGCTGCTCGCAGAAGACGGGCCGTACTGTCTGCTCCACCGACTGACC 543

Qy  535 GGGGCACCTGCAGAAGCAGCCCAGGCAAGCACGACACAGCCAAGCTCAATAAGGGGGTGTTTGGGGAG 594
         |||||||||||||:|||||: || ||||||||||||||:|| |||:||::||| ||||||||||||||

Db  544 GCCCACTTTGGCGCCGCGGGGCATCAGGAGGCCAATAATAACGTGTTGAGCCA 603

Qy  595 AAACAAAACTTGCTGACTGACTACAAAGTAGCCCTCCGGAAGTCGCCCTTCATCGTGTTG 654
         |||||||||| |||||| ||| |||||||:|||||||||:|||| ||||||| |||:|||

Db  604 AAGCCATCAGTGCCCGAGTACAGCAAGGTGCCTCCGTGGGGGGTTCGCTGGCTCCCTCCTC 663
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RESULT 9
AAX84918
ID   AAX84918 standard; DNA; 3736 BP.
XX
AC   AAX84918;
XX
DT   28-SEP-1999 (first entry)
XX
DE   Rat brain specific potassium channel protein coding sequence.
XX
KW   Brain specific potassium channel; central nervous system disorder;
KW   dementia; cerebral ischaemic sclerosis; therapy; probe; ss.
XX
OS   Rattus sp.
XX
PN   WO9937677-A1.
XX
PD   29-JUL-1999.
XX
PF   20-JAN-1999; 99WO-JP00190.
XX
PR   04-DEC-1998; 98JP-0346198.
PR   23-JAN-1998; 98JP-0011434.
XX
PA   (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PI   Miyake A, Mochizuki S, Yokoi H;
XX
DR   WPI; 1999-458683/38.
XX
PT   Potassium channel protein expressed specifically in brain tissue and
PT   method for its production
XX
PS   Example 3; Page 57-59; 63pp; English.
XX
CC   This sequence encodes a rat potassium channel protein, and was used as a
CC   probe to isolate DNA encoding the protein of the invention. The protein
CC   of the invention is a human brain specific potassium channel protein. The
CC   protein is used to treat and investigate disorders of the central nervous
CC   system such as dementia and cerebral ischaemic sclerosis.
XX
SC   Sequence 3736 BP; 706 A; 1210 C; 1000 G; 820 T; 0 other;

Query Match   26.7%;   Score 869.8;   DB 20;   Length 3736;

[DNA sequence alignment between Query (Qy) and Database (Db) with position numbers, not transcribed in full detail]

Best Local Similarity 65.3%;   Pred. No. 6.9e-249;
Matches 1403; Conservative   0; Mismatches 627; Indels 117; Gaps 4;

```
Qy       1 ATGGCCGCCATGCGGGGCCTCCTGCGCCTCCTCAGGAACACCTTCCTGACACCGGCTACG   60
           ||||||| ||||  |||     || |  | ||| |  || ||||
Db     136 ATGGCCGTCATGAAGGGGTTGCTGCGCCTCTTTGCTGCCCCCAAAACACCTTCTGGACACCACT  195

Qy      61 CGCTTCGACGGCACGCAGTAACTTCGTGCTGGGCAACCCCAGGTGGTGGCGGGCTCTTC  120
           |||||| |||||||  || ||||   |||||||| |||     || ||
Db     196 CGCTTTGACGGCACGCAGCAACTTCTTCTGCGCCAATGCCCAGGCCCCAGGGGGTTT  255

Qy     121 CCCGTGGTCTACTGCTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCCCGGGCTGAGGTC  180
           ||| | | ||||||||| |||||  |||||  ||||| ||| |||  || |||
Db     256 CCCATCGTCTACTGCTGCTCTGAGCTCACAGGCTCACAGGCCCGCACCACCGAGGTC  315

Qy     181 ATGCAGCGGGGCTTGCCTCGTCTCCTTCCTTTATGGGCCAGACACCAGTGAGCTCGTCCGC  240
           |||||       | |||  || |||    |  ||||||  || | |||| ||| ||||
Db     316 ATGCAGAAAAACCTGTAGCTGCCGGTTCCTCTATGGCCCAGGACCCAGTGAGCCGGCCGGTG  375

Qy     241 CAACAGATCCGGCAAGGCCCTGGACGAGCAGCAAGGAGTTCAAGGCTGATCCTGTAC  300
           || | || | |      ||||||   |   |||| || |  | |||| ||||
Db     376 CAACGGTTACAAAAAGCCCTGGAGGGCAACCAAGAACACAGAGCTGAAATCTGCTTTAC  435

Qy     301 CGGAAGAGGGGCGTCCCGTTGTGC CTGGATGTGATACCCCATAAAGAATGAGAAA  360
           ||| |  |       |    |   || ||  | |||||    ||  |  ||||
Db     436 CGAAAGGATGGCTCGGCCTTTGTGTCTTCTGGACAATGATGCCCATCAAAAATGAGCTG  495

Qy     361 GGGGAGGTGGCTCTTCCTAGTCTCTCACAAGACATCAGCGAAGCCAAGAACCAGG-  415
           ||||| |  |||| ||    | ||| ||| | ||    |     |     ||||
Db     496 GGGGAAGTCTTCTCCATCTGCACGA GCTCATAGGCGGGCTGAGGGCGGCACCTCTCGAGTG  555

Qy     420 ---GGGCCCCGACAGAGAAGGAGACA------GGTGGTGGCCGCGGTATATGGCCGGG  471
              |||||  |||||  ||||  | |       ||  ||| || | || ||||
Db     556 CTTGGCTTCACCAGGGGAACAATAACATCATAAACCCGGGCGAGAGTTCTCACCAGCGCC  615

Qy     472 GCACGATCCAAAGGCTTCAAGTGCCAACCGGCGGCGGCCCGGCCGCTC-ACCACCTG  531
           |||| ||| ||||| ||||    ||    |||| ||    |  ||| ||||||
Db     616 GGAGCTAGCTCAAGACTTAGGTCCACGAGGAGGCCAGAAGTTCTCACCACCGGTTG  675

Qy     532 TCCGGGCACCTGCGAGAAGCAGCCCAAGGCAGCACAGCTCAATAAGCCGTGTTTGGG  591
           ||||| ||| | ||||  |||| |   ||   ||| | |  | | || | | |
Db     676 ACTGGCCACTTTGGTCGCCGAAGCGGCAAGCCGAATGTAAACGTGTTTGAC  735

Qy     592 GAGAAAACCAAACTTGCCTGAGTACAAAAGTAGCCCCATCCGGAAGTCGCCCTTCATCC  651
           ||| |  |||||   ||  |   | |  ||  ||||  ||  |||  |||||
Db     735 CCAAAGCCATCAGTCGCCGAGTACAAAGTCGCCTGCCGCGCGCCTCCTGGGCCCACACTGTG  795

Qy     652 TTGCACTGTGGGGCCACTGAGCGAGCGCCACCCTGGGTTCATCCGGCTTCATCCTCAT  711
           ||||  | | |||||||     | |  |||||| |||  |||   |||| ||||| |
Db     796 CTCCACTACAGCATCCCAAGGCTGTCTGGGACGGTCTCATCCTCGGTACGTCTCTAC  855

Qy     712 GTGGCGTCACTGTGCCTACAGCGGTGTGTGAGCACAGCAGCCCAGTGCCGGC  771
           |||| ||| | ||| |||    |  | |||| ||  ||||||
Db     856 GTCCGGGTCACCGTGCCCTTACAACGTGCTGATGACGAGACACCCCCATCACG  915

Qy     772 CGCGGGCCCGCCAGCGTCTGTGACCTGCATGGCCTGGAGGTCTCCTCATTGTG  831
           ||| |  | | ||| | |  ||||||| ||||  |  ||   ||||||
Db     916 TCCCAACTTCCGACCACGGTCTTCAACTACTGTGGTACATCGCTCTTCATCCTGGACATGTATG  975

Qy     832 CTGAATTCCGTACCACCATTCGTGTCCAAGTCGGCGGACAGTCGGTGTTTGTTTCCCAAAGTC  891
           || |  ||| || || | |||||| |  |||  ||||||  |||| | | || |||||
Db     976 TTGAACTTCCGACCACCACCTACGGTGTTTCTCGTGTTCTGCGTCCTCGGGCCCCAAAGTCG  1035

Qy     892 ATTTGCCTCCACTACGTCACCACCTTCATGCCTGATGTCATCAGGTGTTTGGGGCGCTGCCCTTG  951
           |||||  | | |||| ||| ||| | |||  ||||
Db    1036 ATTGGCCTCCACTACCTGGCCACCTGGCTCATTGGGACCTTCGTCGGGGCCCATCGCTGGC  1095

Qy     952 GACCTGCTACATGCCTTCAAGGTCAACGTGATCTGCTGAAGACGGTG  1011
           || | |||   |  | |  ||||  || ||| | |||||||||
Db    1096 GACCTGTCTATGTCTTCAACATCACTACTGCTGTACCATCTGTGAAAACCGTG  1155

Qy    1012 CGCCGCTGCTGCGGCCTGGCTCCCCGGCTGGACGTCGTGGCCGTCACCGGCC  1071
           || | ||||||  |||    |  | | |||  |||
Db    1152 GCTGCCGTCAGGGCCTGGCTACTCCGGAGGACCTACCCCGGGACCTACAACCTTCAACCTGCGG  2198
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Qy    1156 CGGCTCCTGCGGTTGCTGAGGGTGCTGCTGCAGAAGCTAGAGCGGTACTCTCAGTGCAGCGCG  1215
           |||||||||||||| | ||||||||||| ||||| || || ||||
Db    1072 GTGGTGCTGACAACTGCTGTTCCTGACACCGGCTACG  1131

Qy    1216 GTGGTGCTCACCGCTGCTCATGTCCGTCTTGCACTCGATGGCCTGCGTC  1275
           ||||||||  ||||||| ||| ||| | |||||||| |||||| |||
Db    1132 TGGTTTACATTGGCCAGCGGAGATCGAGAGCAGCAGCGAATCCGAGCTGCCTGAGATTGGC  1191

Qy    1276 TGGTATGTCATCGGGCAGGGAGGATGGAGGCCAATGACCCGTGTCTGGGGACATTGGT  1335
           ||| | |   |||| ||| | |||| |||| ||||  |||  | |||||||||
Db    1192 TGGCTGCGAGGAGCGGCCGCCGGACTCCGAGACTCCTACTACCTGTGGGGCGGGAGGCCA  1251

Qy    1336 TGGTTCATGAGCTGGTAAGCGGCTGGAGGAGCCTTATGTCAATGGCTC-------  1385
           ||  || ||  | ||  |||| ||  |||| |||  | | ||||
Db    1252 GCTGGGAGGGAACAGTCTCCGGCCACAGAGTGACAACTGCAGCAGCGAGCCAACGGG  1311

Qy    1386 --------------------------------  1385
Db    1312 ACGGGGCTGAGCGCTGGGCGGCCCGTCGCTGGGCAGGCTACATCACCTCCCTCTAC  1371

Qy    1386 -------GCCGGTGGAGCCAGCGTCACCAGTCGATCGTGAC  1431
                  ||| | || |||  ||| | ||||| | || |
Db    1372 TTCGCACTCAGGACGCCTCACCGGCTGGGCTTCGGCAACGTCTCCGCAACACGGACACC  1431

Qy    1432 TTCGCACTCAGGCCTCCATCTGCACCATGCTGCGCGCCCCTGATGCACGCGTGGTGTTT  1491
           ||||| ||||||| ||| | | |||||  | |  | ||    || |||| | | |
Db    1432 TTCACGCTGAGCAGCTCACCAGTGCCTGATGCGACGA GCTCATAGGCGCACTGCGGTGTGTTT  1491

Qy    1492 GAGAGATCTTCTCCATCGTCACCATGCTGCACATGCTGCAGG-  1551
           ||||||||||||||  ||| |||| ||| | |||
Db    1492 GAGAAGATCTTCTCCATCTGCACGAGCTCGATAGGCGGGCTGAGG  1551

Qy    1492 GGGAACGTGACCGGCCATCATCCAGCGGCCATGAGTACCCCGGCTTTCTGTGTACCACAGCCGC  1551
           |||||  |||| || | |  ||| |||   ||   | ||| |  ||| | |||||||
Db    1552 CGGAATGTCACACGCCATCACCATCCACCAGCGTACTCCGCGTCTACCACCAGCCGC  1612

Qy    1552 ACGCGGCAACCTGCGCGACTACATCCGGCTACATCCACCACCGTATCCCCAAGCCCTCAAGCAGCGC  1611
           | | || | ||| |  || |  ||| ||||| | ||| ||||   | ||||||||
Db    1612 ATGAAGGATCTCAAGGACTTCATCCGAGTGCATCTCTGCGCCCCCACTCAGCACCACGCGC  1671

Qy    1612 ATGCTGGAGTACTTCCAGCCAGCACCTGGGCGTGACCATGGGCGTGACAACAATGGCATCGGCGAGCTG  1671
           ||| || |||| ||| |||  | ||| ||||| | |||||||||  |||||
Db    1672 ATGCTCGAGTACTTCCAGACTACATGGGGCCGTCAACGACTAGGGCCATCGATGCCGTCAACGAGTTA  1731

Qy    1672 CTGCAGAGCCTCCGACGAGCTCGCGCCGCAGAGCTCGCAGATCGCCATCGCACCTGACAAGGAGGTC  1731
           |||||| |||  | |||||| || | | |  ||| ||  | |||  ||||| |||
Db    1732 CTGCGTGACTTCCCGGATGAGTCGCCGGAGGTCGTGACATCGCCATCGTCAACTGAATCGGGAGATC  1791

Qy    1732 CTGCAGTCGTTCCACTGTTGAGGCCGCGCCAGCCGCCAGCAAGCAGCAGGGTGCTGCGCTCTGGCC  1791
           |||||| |  || | | |||||| |  |||||||||  | ||||||
Db    1792 CTGCAGCTGCCTTTGTTGTTGGAGCAGCAAGCAGGGCTGCGCCTTCGTGCCTCCCTCTCCCTGCAC  1851

Qy    1792 CTGCGGGCCGCCGATGCCCTCGTCGCACGCGATGACGACGACCCCCCATCACGCAG--------  1851
           || | |  ||  | | ||||   |  ||| |  |||| |||||
Db    1852 ATCAAGACCTCATTTTGTGCTCCTGGGAGTTGCTACCGGTGATGACGAACACCGGTGCCATCATC  1911

Qy    1852 GCCCTCTACTTGTCGTCGGCCGTGGAGGTGGCTCCATGGGAGGTGGCACCCGTGCTCTGCC  1911
           ||||| ||||  || || |||  |||||||  |||||||||| ||||||
Db    1912 GCACACTACTATGTGTCAGTGTTGTCTTGGGAGATGGCTGGGAGCTGCGAGGGAGCTGGCAC  1971

Qy    1912 ATCCTAGGGAAGGGCGACCTGATCGGCTGTGAGCTGCGCGGCGGGGAGCCAGCAG--------  1962
           ||||  | || || |||||| || | ||| |||||||||  | |||  ||||
Db    1972 ATCCTTGAAAAGGGGCACTTGATTGGGGCAGACATCCCTGGTGGGCAGGAGGCCTGGG  2031

Qy    1963 -------GTGGTAAAGCCAATGCGGTGAAGGGGCTGAAGGGGCTGAAGACGTGAAGACTACTGCGGC  2007
                  |  |  | | | |  ||||||  | | ||||||
Db    2032 GCAGGGCAGGGCTGCGTGCTGCAGGACACTGAGTGGGCAGACACTCCCGAGTTGGGCAGGAGCCTGGGC  2091

Qy    2008 CTGCAGTGTCTGCAGACGCTTCAAGGTCAACGTGATCTGCTGAAGACGGTG  2067
           |||||| | ||||||| || | |||| || | |  ||  || | ||
Db    2092 CTGCAGCTGTCTGAGCAGCCGAGGGCTGGCCGAGGGTCCTTCGGTTGTTATCCGGAATATGTG  2151

Qy    2068 CGCCGCTGCTGCGGCCTGGCTCCCCGGGCTGGACGTACTCAGCTACAACCGTG  2114
           || | |||||||  || || ||||||||  || |  || |||| | |||
Db    2152 GCTGCCTTCAGGGGCTGGCTGGCCTCACCCCCGGGACCTACAACCTTCAACCTGCGG  2198
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RESULT 10
AA250454
ID   AA250454 standard; cDNA; 1132 BP.
XX
AC   AA250454;
XX
DT   18-MAY-2000 (first entry)
XX
DE   Human potassium channel molecule ERG-LPl; partial cDNA.
XX
KW   Human; potassium channel molecule; ERG-like protein 1; partial ERG-LP1;
KW   neuroprotective; antiParkinsonian; anticonvulsant; antidepressant;
KW   neuroleptic; nootropic; treatment; CNS disorder; central nervous system;
KW   potassium channel mediated disorder; epilepsy; Alzheimer's disease;
KW   Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia;
KW   chromosome 1q11-13; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..262
FT                   /tag= a
FT   mat_peptide     263..1132
FT                   /tag= b
FT                   /product= "Partial ERG-LP1"
FT                   /transl_except= (pos:1031..1033, aa:Arg)
FT                   /note= "This region is specifically claimed"
XX
PN   WO200005346-A1.
XX
PD   03-FEB-2000.
XX
PF   21-JUL-1999;  99WO-US16752.
XX
PR   21-JUL-1998;  98US-0119855.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Curtis RAJ;
XX
DR   WPI; 2000-182682/16.
DR   P-PSDB; AAY44906.
XX
PT   Novel gene encoding potassium channel molecule useful in treating
PT   central nervous system disorders such as Alzheimer's disease, multiple
PT   sclerosis, and schizophrenia -
XX
PS   Claim 2; Fig 5; 144pp; English.
XX
CC   The present sequence is a cDNA encoding partial ERG-like protein 1
CC   (ERG-LP1) which is a member of ERG potassium channel family. This
CC   sequence is derived from a human EST (expressed sequence tag).
CC   IMAGE clone 37299. ERG-LP1 is expressed exclusively in the brain.
CC   Highest expression is found in cortical regions, hippocampus, caudate
CC   and amygdala. ERG-LP1 gene was mapped to human chromosome 12q1-13,
CC   between markers WI-7107 and WI-6327.
CC   The protein functions as a potassium channel modulator and
CC   has neuroprotective, antiParkinsonian, anticonvulsant, antidepressant,
CC   neuroleptic and nootropic activities. The present sequence is
CC   useful for treating several potassium channel mediated disorders (CNS
CC   disorders) such as Alzheimer's disease, Parkinson's disease, multiple
CC   sclerosis, epilepsy, depression, schizophrenic disorders and amnesia.
XX
SQ   Sequence 1132 BP; 189 A; 376 C; 379 G; 188 T; 0 other;

Query Match             26.0%;  Score 844.4;  DB 21;  Length 1132;
Best Local Similarity   99.9%;  Pred. No. 2.5e-144;
Matches  845;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy       1 ATGCGGCCATGCGGGGGCCTCCTGGCGCCTCAGAACACCTTCCTGGACACCACCATCGCTACG  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     263 ATGCGGCCATGCGGGGGCCTCCTGGCGCCGCAGAACACCTTCCTGGACACCACCATCGCTACG  322

Qy      61 CGCTTCGACGGCACGCACGCACAGTAACTTCGTGCTGGGCAACGCCCAGGTGGCGGGCTCTTC  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     323 CGCTTCGACGGCACGCACGCACAGTAACTTCGTGCTGGGCAACGCCCAGGTGGCGGGCTCTTC  382

Qy     121 CCGTGGTCTACTGGCTGCTGATGGCTTCGTGACCTCACGGGCTTCCCGGGCTGAGGTC  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Dt     383 CCGTGGTCTACTGCTTCTGTGACCTTCACGGGCTTCCCGGGCTGAGGTC  442

Qy    181 ATGCAGCGGGGCTGTGCCTGCCTTCCTTTATGGCCAGACACCAGTGAGCTCGTCGGC  240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    443 ATGCAGCGGGGCGTGTCCCTGCCTTCCTTTATGGCCAGACACCAGTGAGCTCGTCGGC  502

Qy    241 CAACAGATCCGGACGAGCCCTGGACGACGACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC  300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    503 CAACAGATCCGCAACGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC  562

Qy    301 CGGAAGAGCGGGGCTCCCGTCTGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA  360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    563 CGGAAGAGCGGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA  622

Qy    361 GGGGAGGTGGCTCTCTTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG  420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    623 GGGGAGGTGGCTCTCTTCTTCCTCAGTCTCTCCACAAGGACATCAGCGAAACCAAGAACCGAGGG  682

Qy    421 GGCCCCGACAGATGGAAGGACAGCAGGTGGTGGTCCGGCGCCGATATGGCGGGCACGATCC  480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    683 GGCCCCGACAGATGGAAGGACAGCAGGTGGTGGTCCGGCGCCGATATGGCGGGCACGATCC  742

Qy    481 AAAGGCTTCAATGCCAACCGGCGGGCCGTGCTTCTACCACCTGTCCGGCAC  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    743 AAAGGCTTCAATGCCAACCGGCGGGCCGTGCTTCTACCACCTGTCCGGCAC  802

Qy    541 CTGCAGAAGCAGCCCTACAGCGTGTGTGAGCACAGCGGGTGTTGGGAGAAACCA  600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    803 CTGCAGAAGCAGCCCTACAGCGTGTGTGAGCACAGCGGGTGTTGGGAGAAACCA  862

Qy    601 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTGCCCTTCATCCTGTTGCACTGT  660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    863 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTGCCCTTCATCCTGTTGCACTGT  922

Qy    661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCCACACTCTATGTGGCTGTC  720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    923 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCCACACCTCTATGTGGCTGTC  982

Qy    721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGCAGGCCCAGTGCCGCCCGGGGCCCG  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    983 ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGCAGGCCCAGTGCCGCCCGGGGCCCCG  1042

Qy    781 CCCAGCGTCTGACCTGGCGGAGGTCCTTCATCCTTGACATTGTGCTGAATTTC  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1043 CCCAGCGTCTGACCTGGCGGAGGTCCTTCATCCTTGACATTGTGCTGAATTTC  1102

Qy    841 CGTACC  846
          ||||||
Db   1103 CGTACC  1108
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RESULT 11
AA293334
ID   AA293334 standard; cDNA; 3742 BP.
XX
AC   AA293334;
XX
DT   04-JUL-2000 (first entry)
XX
DE   Rat elk1 potassium channel gene.
XX
KW   Elk1; elk2; eag1; eag2; erg1; potassium channel; membrane protein;
KW   drug screening; hypertension; renal failure; diabetes insipidus;
KW   diabetic nephropathy; hypothyroidism; goiter; hypoparathyroidism;
KW   pancreatic insufficiency; diabetes mellitus; cystic fibrosis;
```

```
KW   sialorrhea; salivary insufficiency; membrane potential; current flow;
KW   ion flux; transcription; signal transduction; assay; detection;
KW   rat; ss.
XX
OS   Rattus rattus.
XX
FH   Key             Location/Qualifiers
FT   CDS             53..3360
FT                   /tag= a
FT                   /product= Elk1 potassium channel protein
FT                   /note= "Whilst this sequence is cross referenced to
FT                   a GENESEQ protein file, this nucleotide
FT                   sequence as it stands does not accurately
FT                   encode the protein contained within that
FT                   file.  This sequence has been reproduced
FT                   accurately from the patent application
FT                   specification although for it to accurately
FT                   encode the protein described in GENESEQ
FT                   record AAY83028, it requires an Adenosine
FT                   nucleotide between nucleotide positions
FT                   2048 and 2049 of this indexed sequence"
XX
PN   WO200012546-A1.
XX
PD   09-MAR-2000.
XX
PF   31-AUG-1999;    99WO-US19902.
XX
PR   31-AUG-1998;    98US-0098413.
XX
PA   (UYNY ) UNIV NEW YORK STATE RES FOUND.
XX
PI   McKinnon D, Dixon JE;
XX
DR   WPI: 2000-256585/22.
DR   P-PSDB: AAY83028.
XX
PT   Novel mammalian potassium channel genes and polypeptides encoded by
PT   them for screening drugs useful for treating diseases such as
PT   hypertension, acute renal failure, diabetes insipidus and
PT   hypothyroidism -
XX
PS   Claim 1; Page 80-8?; Page 102pp; English.
XX
CC   Potassium channel genes e.g. elk1, elk2 or eaq2 are useful for
CC   identifying modulators which are useful for treating hypertension,
CC   acute and chronic renal failure, diabetes insipidus, diabetic
CC   nephropathy, hyperthyroidism, goiter hyperparathyroidism,
CC   pancreatic insufficiency, diabetes mellitus, cystic fibrosis,
CC   sialorrhea, salivary insufficiency. The availability of the gene
CC   sequences provides a tool for research into the physiobiological
CC   characteristics of the various genes and proteins for potassium
CC   channels including the development of medicines effective for
CC   treating disease conditions associated with mutations or defects in
CC   potassium channels and the screening of drugs to ensure that
CC   potassium channels are not blocked or physiologically affected by
CC   those drugs. The channel proteins encoded by these genes are also
CC   useful themselves as reporter molecules in assay and detection
CC   systems to measure changes in potassium concentration, membrane
CC   potential, current flow, ion flux, transcription, signal
CC   transduction, receptor-ligand interaction and second messenger
CC   concentrations.
XX
SQ   Sequence 3742 BP; 1034 A; 903 C; 880 G; 925 T; 0 other;
```

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Query Match             24.4%;  Score 794.4;  DB 21;  Length 3742;
Best Local Similarity   63.2%;
Matches 1340;  Conservative  0;  Mismatches  686;  Indels  94;  Gaps  4;

Qy      1 ATGCCGGCCATGCGGCGGGGGCCTTCCTGGCCGCCTCAGGAACACCTTCCTGGACACCGCTACG 60
          ||||||| ||| ||| ||| |||||||| |||||||||||||||||||||  ||||| | ||
Db     53 ATGCCGGTTATGAAAGGATTGCTGGGGCCACAGAACACCTTCCTGGACACTATTGCCACC 112
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XX
DT   18-MAY-2000  (first entry)
XX
DE   Human potassium channel molecule ERG-LP2 full-length cDNA.
XX
KW   Human; potassium channel molecule; ERG-like protein 2; ERG-LP2;
KW   neuroprotective; antiParkinsonian; anticonvulsant; antidepressant;
KW   neuroleptic; nootropic; treatment; CNS disorder; central nervous system;
KW   potassium channel mediated disorder; epilepsy; Alzheimer's disease;
KW   Parkinson's; multiple sclerosis; depression; schizophrenia; amnesia;
KW   chromosome 3p21.3-24.3; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..195
FT                   /tag= a
FT                   196..3519
FT   CDS             /tag= b
FT                   /product= "ERG-LP2"
FT   3'UTR           3520..5107
FT                   /tag= c
XX
PN   WO200005346-A1.
XX
PD   03-FEB-2000.
XX
PF   21-JUL-1999;  99WO-US16752.
XX
PR   21-JUL-1998;  98US-0119855.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Curtis RAJ;
XX
DR   WPI; 2000-182682/16.
DR   P-PSDB; AAY44907.
XX
PT   Novel gene encoding potassium channel molecule useful in treating
PT   central nervous system disorders such as Alzheimer's disease, multiple
PT   sclerosis, and schizophrenia
XX
PS   Example 1; Fig 8; 144pp; English.
XX
CC   The present sequence is a cDNA encoding full-length ERG-like protein 2
CC   (ERG-LP2) which is a member of ERG potassium channel family. This
CC   sequence is a result of additional sequencing of clone jlhbaa042h05 which
CC   was obtained from human brain library. ERG-LP2 gene is mapped to
CC   human chromosome 3p21.3-24.3, between markers WI-4218 and RP_L15_1. It
CC   is predominantly expressed in the brain.
CC   The protein functions as a potassium channel modulator and
CC   has neuroprotective, antiParkinsonian, anticonvulsant, antidepressant,
CC   neuroleptic and nootropic activities. The present sequence is
CC   useful for treating several potassium channel mediated disorders (CNS
CC   disorders) such as Alzheimer's disease, Parkinson's disease, multiple
CC   sclerosis, epilepsy, depression, schizophrenic disorders and amnesia.
XX
SQ   Sequence 5107 BP; 1486 A; 1137 C; 1092 G; 1391 T; 1 other;
```

Query Match　　23.4%;　　Score 761.2;　DB 21;　Length 5107;
Best Local Similarity　62.2%;　　Pred. No. 3.8e-129;
Matches 1319;　Conservative　　0;　Mismatches 708;　Indels　93;　Gaps　4;

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Qy      1 ATGCGGGCCATGCGGGGCCTCTGCGGCCTCCTGACACCATCGCTACG  60
          ||||||| || | | ||||||| | |||||||||||||||||| ||| ||
Db    196 ATGCGGGTTATGAAAGGATTACTGGCGCCGCAAAACACCTTCCTGACACACCGCCACC 255

Qy     61 CGGTTGGACGGCGCACGCACAGTAACTTCGTTGCTGGGTCAAGCGCCAACGCCGTGGGGGCCTCTTC 120
          || | ||||| ||| | | |||| ||||| |||||||||||||||||||
Db    256 CGTTTGACGGGACAACCATAGCCAACTTCCATCCTTGCCATGCCAGTTGGCTAAGGGTTC 315

Qy    121 CCCGTGGTCTACTGCTCTGATGGCTTCGTGACCTCACGGCGTCTTCCCGGGCTGAGGTC 180
          ||||| | |||||| || |||||||||| || || ||| |||| | |||||| || |||
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RESULT 12
AA250455
ID   AA250455 standard; cDNA; 5107 BP.
XX
AC   AA250455;

Db   1181 ... ATTGGAAAAATGGAGAGGAGGACAACAGCCTTCTCAGTGGAAGTCGGTTGCTTCAC 1240
Qy   1201 GAGCTGGCCGCCGACTGGAGACTCCCTACTACCTGGTGGGCCGGAGGCCAGCTGGAGGG 1260
Db   1241 GAGCTGGAAAGAGACTGGAATCTCCGTACTAC--------- 1273
Qy   1261 AACAGCTCCGCCAGACTGACAACTGCAGCAGCAGCAGCGAGGCCAACGGGACGAGGGGCTG 1320
Db   1274 ------------------------------GGCAACC 1279
Qy   1321 GAGCTGTGGCGGCGGCCCGTCGCTGCGCAGCGCCTACATCACCTCCTCACTTCGCACTC 1380
Db   1280 AACAGCTGGGCGGCGGGCCCGTCCATCCGCAGTGCCTATATCGCAGCCTTGTTACTTCACTCTC 1339
Qy   1381 AGCAGCCCTCACCAGCGGTGGCTTCGGCAACGTGTCCCGCCAACACGGACACCGAGAAGATC 1440
Db   1340 AGCAGCCTCACCAGCGTGGGATTTGGGAATGTCTCCGCTAACACGGATGCAGAGAGAATC 1399
Qy   1441 TTCTCCATCTGCACCATGCTCATCGGGCGGCCTGATGCACGGGTGGTGTTTGGGAACGTG 1500
Db   1400 TTCTCCATCTGTACCATGTTGATTGAGGAGCCCTGATGCATGCTTGGTA-TTGGGAATGTG 1459
Qy   1501 ACGGGCCACATCATCCAGGCACGGCCATGTACGCCCGCGTTCTGTACCAGCCGCACGCGCGAC 1560
Db   1460 ACTGCCCATCATACAGAGAATGTACTCTAGATGGAGCCTGTACCATACTAGAACCAAGGAC 1519
Qy   1561 CTGCGGGACTACATCCGGCATCCCCGTATCCCCAAGCACGCGCATGCTGGAGG 1620
Db   1520 CTAAAAGGACTTCATCCGTGCATCACCGTGCCCAGCAACTCAAGCAGGGATCCTTGAG 1579
Qy   1621 TACTTCCAGGCCACCTGGGCGTGAACAATGACGCATGACACCGAGCTGCTCGCAGAGC 1680
Db   1580 TACTTTCAGACAACTTGGTGTCTGTCAACAATGGAATAGATTCAAATGAGCTTTGAAAGAC 1639
Qy   1681 CTCCCTGACGGAGCTGCGCGCAGACATGCCCATCGACACCTGCACAAGGAGGTCCTGCAGCTG 1740
Db   1640 TTTCCAGATGAGCTGCGCTCTGACATCCATCTGAACAGAGGAGATCTTACAGCTG 1699
Qy   1741 CCACTGTTGAGGCGGCCAGCCGGCTGCCTGCGGCCACTGGTCTCTGCCCCTGCGGGCC 1800
Db   1700 TCCCCTGTTTGAATGTGCTAGCCGGGGTCTGCGGGGCTGTCTGTCTCTCCATATATAAAACC 1759
Qy   1801 GCCTTCTGCACGGGCGGGGAGTACCTACCTCCACCAAGGCGATGCCCTGCAGGCCTCTAC 1860
Db   1760 TCATTCTGTGCCCCAGGAGAGTATCTGCTGCGCAGGGAGAGTGCGTTGCAGGCCATCTAC 1819
Qy   1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGCACCGTGCTCCCCATCCTAGGG 1920
Db   1820 TTCGTGTGCTCAGGCTCATGGAGGTTCTTAAAGACACAGCATGGTGTTGGCTAATCTAGGG 1879
Qy   1921 AAGGGCGACCTGATCGGCTGTGAGCTGCCCCGGGGAGCAGTGGTAAAGGCCAATGCC 1980
Db   1880 AAGGGGGGATTTAATTGGAGCAAATTTATCAATTAAAGACCAAGTGATCAAGACCAACGCT 1939
Qy   1981 GACGTGAAGGGCTGACCTACTGCGTCTGCAGTGTCTGCGCCTGCCTCCACGAC 2040
Db   1940 GACGTGAAGGCTCTGACCCTACTGGTCGCATCATCCTGAAAGTCTCTTTGAG 1999
Qy   2041 AGCCTTCGCGCTGTACCCCGAGTTGCCCGCGCTTCAGTCGTCGGCCC--CCCAGGGGGAGGTC 2100
Db   2000 GTGCTGGGCCTTTACCCAGAGTACGGACACACAAATTC-GTAGAAGACATCCGCAGACACCTC 2058
Qy   2101 AGCTACAACCTTGGGTGCTGG 2120
Db   2059 ACATACAACCTTCGAGAGAGG 2078
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Db   316 CCCAATAGTCTACTGTTCCGATGGCTTCTGCGAGCTTGCTGTGGAATTGCCGAACTGAAGTC 375

Qy   181 ATGCAGCGGGGCTGTGCCTGCCTCCTTATGGCCAGACACCGAGCTGAGCTCGTCCGC 240
         |||||  |||  |  |||  |||  | ||||  |  |||  ||| |||||  | ||||
Db   376 ATGCAGAGAGAGTTGTAGCTGCAAGTTCTTATTTGGGGTTGAAACCAATGACAACTGATG 435

Qy   241 CAACAGATCCGCAAGGCCCTGACGAGCACAAGGACGAGTTCAAGGCTGAGCTGATCCTGTAC 300
         | | | |||| ||| ||||| |  |  || |  | ||| ||||  | ||||| |  |
Db   436 CTTCAAATAGAAAAGTCACTGGAGAGAAAACAGAAATTCAAAGAGAAATTA GTTCTAC 495

Qy   301 CGGAAGAGCGGGCTCCCGTTCTGTGTCTCCTGATGTGATACCCATAAAGATTGAGAAA 360
         |||  |  | | |||  |  |  |||  |||| || | | | ||| | |  ||||||
Db   496 AAGAAAAACGGGTCTCCATTTTGGTGCCTACTGCGATATTGTTCCCATAAAGAATGAAAAA 555

Qy   361 GGGGAGGTGGCTCTCTTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420
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Db   556 GGAGATGTAGTACTTTTCTGGCCTCGTTCAAAGATATAACAGATA CAAAAGTGAAGAT 614

Qy   421 GGCCCCACAGATGGAAGGAGACAGGTGTGGCCGGCCGATATGGCCGGGCACGATCC 480
         |||  || ||| || |   |  | ||  |||  |||||  |||   || ||| |
Db   615 TACTCCAGAAGAATAAAAAAAGAAGACAAGTCAAAGGAAGAATCAAGAGACAGCAGGGACCCA--- 671

Qy   481 AAAGGCTTCAATGCCAACCGGCGGGACGTGCTCTACCACCTGTCCGGGCAC 540
         |||  |    | | ||   |||  |||  |||  |||||||   ||| |||
Db   672 ----CTTTGACTCAGCCCGGGAGACGAGCAGTCGAGCAGTCCTTTATCACATCTCTGGGCAC 726

Qy   541 CTGCAGAAGCAGCCCAAGGCACACAGCTCAATAAGGGGGTGTTTGCGGAGAAAACCA 600
         |||  ||    |  |||| |||||   |  | | | ||  |  |  |  ||
Db   727 CTGCAAAGAAGAGAGCAAAATTGAAAATAAATAAACAAATGTTTTTGCAGATAAATCAGTCTTGAGAC 785

Qy   601 AACTTGCCTGAGTACAAAGTAGCCGCAATCGGGAGCGCCCTTCATCCTGTTGCACTGC 660
         ||  | |  | |  | | ||     | |||| | | |||  | | |||  |  |||||
Db   786 GCATTCCGAGTATAAAGTTTCTGATGCAAAAGTCCAAAATTCATACTTCCGCATTTT 846

Qy   661 GGGCCACTGAGAGCCACCTGGGATGGCTTCATCCTCGCCCACACTCTATGTGCCGTC 720
         |||  |||  |  |  || |  |  |||||  |   |  |  ||  | ||||  | ||
Db   847 AGCCACTTTAAAGCTGGCTGGGACTGCCTTATTTTGTTGGCAACGTTTTTGTTGCTGTG 906

Qy   721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCAGCCACGGGCAGGGAGGAGCCCCCCG 780
         ||||  |  |  |  | ||  || | |  | ||| ||  ||  ||||  | ||||||
Db   907 ACTGTACCTTACAACGTTTGCTTTATGGCCAATGACGACCTGTCCACAACTCGGAGC--- 963

Qy   781 CCCAGGTCTGTGACCTGGCCGTTGGCGTCCTTCATCCTTGACATTGCGGCTGAATTC 840
         |||| || |  | |  ||| | || | |  | | ||    |  | | |  | ||  |
Db   964 ACAACCCCAGTGACATGACATGCAGGTCAACGTTCTTTTTATAGATATTATTTAAAATTC 1023

Qy   841 CGTACCACATTCGTGTCCAAGTCGGGCCAAGTCGGGCCAGGTGTGTTTGCCCCCAAAGTCCATTGGCCC 900
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Db  1024 CGAACAACTTATGTCAGCAAGTCTGGGCAAGTTATCTTGAAGCAAGATCAATTGCAATTTGCCATC 1083

Qy   901 CGCCTGCTGCCTCACCACCTGGTTCCGCGGCTGGACCTGGTCATCGGACGCTGGTACTGGGCTGCTA 960
         || ||||| |   |   ||   |  ||  | || |   ||  ||||  |  || ||| |  ||||
Db  1084 CACTATGTCACAACCTGGTTCATTGGAGCCGATGCTTTAACCTACTG GATCTCAGTGTATCATCTTCCG 1143

Qy   961 CATGCCTTCAAGGTCAACGTGTACTTCGGGGCCACTGCTGAAGACGGTGCGGCCTTCATG 1020
         || |  ||||| |  |||  | || ||  ||| | ||| || | | |||||| |||||
Db  1144 TATGCTTTCAAGGTCACACTGGTGTCTCTCGCATCTTCTCTAAAGACACAGGTGCGCCCTCTTG 1203

Qy  1021 CGCCTGCTGCCTGCTTCCGCGGCTGCATGGGGTGCTGG 1120
         ||  || | ||  | ||| | ||   | ||||| ||||
Db  1204 CGTCTTTGCGCTCGTCTCTGCAGAAGTTAGACCGCTATTCCCAACACAGTACTACGTCGCCCTG 1263

Qy  1081 ACACTGCGCATGGCCGTGTTCGCGTCGCTGCCACTGGGTCGCGCCACTGGCTCTGGTTTAC 1140
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Qy  1141 ATTGGCCAGCCGGGAGATCGAGAGCAGCAGCAGAATCCAGCTGCTCGAGATTGGCTGGCTGCAG 1200
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Qy  1201 GAGCTGGCCCCGCGACCCGGATGGGTGGCCCGGAGCCAGCTGGAGGG 1250
         ||  || | | | || |   | | |||||| ||||||||| ||||||
Db  1384 GAGTTGGGAAAGAGACTGAATCTCCATACTAT------ 1416
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Db  1261 AACAGCTCCGGCAGCGGGCTGTGCCTGCCTCCTTACTTCGCACTC 1320
                                                          ||
Qy  1417 --------------------------------------GGCAAC 1422

Qy  1321 GAGCTGCTGGGCGGCCCCGTGCGCTCGCAGCGCGCTTACACACTCCCTCCTTACTTCGCACTC 1380
         ||  |  || |||  |  ||   |  |  |  |  | |  |||     ||||  || ||  |||
Db  1423 AATACCTTGGGGGCCCGTCGATCCGAAGTGCCTATATTGCCGGCTTTCACGCTG ACGCTG 1482

Qy  1381 AGCAGCCTCACCGTGGGCTTCGGCAACGTGTCCGCAACACGGACACCGAGAAGATC 1440
         |||||||| ||||||| ||||| ||||||||| ||  ||  | ||||  ||||||||
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Qy  1441 TTCTCCATCTGACCATGCTCATCGGCCCGCCCCTGATGCACGCGGTGGCGTGTTGGGAACGTG 1500
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Qy  1501 ACGGCCATCATCCAGCGCATGTACGCCCCGCGTTCTGTACCCACAGCGACGATCTAAGGAT 1560
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Qy  1561 CTGCGGACTACATCCGCATCCACCGTATCCCAAGCGCCCTCAAGCAGCGCCATGCTGGAG 1620
         |||   ||| ||   |  |  ||  |||   |  || |   ||||  |  |  ||||||||
Db  1663 CTGAAAGATTCATCCGTGTCCAATCACTTGCCCCAACAACTCAAGCAGGATGCGTCGAA 1722

Qy  1621 TACTTCCAGGCCACCTGGGCCGGTGAACAATGGCATCGAACACCGAGGCTGCTGCAGAGC 1680
         |  |||  ||| |   |  |  ||  | | | | | |  | | ||  | | | ||||||||
Db  1723 TATTTCAAACAACACCTGGTCAGTCAACAATGGAATAGATTCAAATGAGCTTTTGAAAGAC 1782

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Db  1783 TTTCCAGATGAACTGCGTTCTGACATCATCATGACCTTGAACAAGGAGATCTTACAGTTG 1842

Qy  1741 CCACTGTTTGAGGCCGGCCAGCCGCTGCCGGCCACTGTCTCTGGCCCTCCGGCCCC 1800
         | | ||||| || ||   |  || | | ||  | | |  | |  ||||  | |||||
Db  1843 TCCCTTTTTGAATGTGCCAGCCGGCGGGGCTCCTGCTCTCTCTACACAATCAAAACC 1962

Qy  1801 GCCTTCTGCACGCGCCGGCTGGGAGTACCTCATCCACCAAGGCGATGCCAGGCCCTCTAC 1860
         || | | |  |  |  ||| | | || | ||   | |  |  |||  ||| |  || ||||
Db  1903 TCTTTCTGTGTCTCCGGGGAGTATCTGCTGCGGCTGAGGAGATGGCTTTGCAGGCCATCTAC 1962

Qy  1861 TTTGTCGTCCTCTGGCTCCATGGAGCTCCATCCTTGACATTGCGTCTCGCCATCCTAGG 1920
         ||| |  ||   | | ||  | |  | |||  |  |  |  |  | | |  ||  ||||
Db  1963 TTTGTATGTCTCGGGCTCCATGGAGTTCTTAAAGAGAGTTCTGGCTATTCTTGGG 2022

Qy  1921 AAGGGCGACCTGATCGGCTTGAGCTGCGTGTGCAAGCAGGTGCTAAAGGCCAATGCC 1980
         ||||| |  | | | | ||   ||| | |  | | | || | ||||  |||||||||
Db  2023 AAAGGGGATTTAATTGGAGCAAATCTATCAATTAAGGACGAATCGATCAAGACCAATGCA 2082

Qy  1981 GACGTGAAGGGCTTGACGTACTGCGTCCTGCAGTTGTCTGACCTGCCTGCACGAC 2040
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Db  2083 GATGTAAAGGCTTTAACCTACTG GATCTCCAGTGTATCATCTTGAA 2142

Qy  2041 AGCCTTGGCCGTGTACCCCGAGTTGCCCGCGGTCCCGAGGGGGAGCTC 2100
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Db  2143 GTGCTAGACCTTTACCCGAGAATATGCTCACAAATTCGTGAAGCATGCAGCATTCAGCGATGACCTC 2202

Qy  2101 AGCTACAACCTGGGTGCTGG 2120
         |||||||||| |  | ||||
Db  2203 ACATACAACCTCCGAGAAGG 2222
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RESULT 13
ABA20014
ID   ABA20014 standard; DNA; 10579 BP.
XX
AC   ABA20014;
XX
DT   23-JAN-2002 (first entry)
XX
DE   Human nervous system related polynucleotide SEQ ID NO 12345.
XX
KW   Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;

KW	immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;			
KW	antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;			
KW	antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;			
KW	antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;			
KW	antiparasitic; cardiant; immune disorder; cardiovascular disorder;			
KW	neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.			
XX				
OS	Homo sapiens.			
XX				
PN	WO200159063-A2.			
XX				
PD	16-AUG-2001.			
XX				
PF	17-JAN-2001; 2001WO-US01334.			
XX				
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		PR	17-NOV-2000; 2000US-0249297.
		PR	17-NOV-2000; 2000US-0249299.
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		PR	01-DEC-2000; 2000US-0250391.
		PR	01-DEC-2000; 2000US-0251160.
		PR	05-DEC-2000; 2000US-0251030.
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		PR	05-DEC-2000; 2000US-0256719.
		PR	06-DEC-2000; 2000US-0251479.
		PR	08-DEC-2000; 2000US-0251856.
		PR	08-DEC-2000; 2000US-0251868.

PR   08-DEC-2000; 2000US-0251869.
PR   08-DEC-2000; 2000US-0251989.
PR   08-DEC-2000; 2000US-0251990.
PR   11-DEC-2000; 2000US-0254097.
PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA, Barash SC, Ruben SM;
XX
DR   WPI; 2001-541565/60.
XX
PT   Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating nervous system
PT   cancers and metastases -
XX
PS   Disclosure; SEQ ID NO 12345; 170lpp + Sequence Listing; English.
XX
CC   The invention relates to novel genes (ABA11004-ABA21534; and proteins
CC   (ABB14678-ABB18001) useful for preventing, treating or ameliorating
CC   medical conditions e.g. by protein or gene therapy. The genes are
CC   isolated from a range of human tissues disclosed in the specification.
CC   The nucleic acids, proteins, antibodies and (antagonists are useful
CC   in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC   and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC   marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC   (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC   colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC   (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC   epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC   and parasitic infections.
CC   Note: The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 10579 BP; 2298 A; 2894 C; 3129 G; 2256 T; 0 other;

Query Match   18.5%; Score 601; DB 22; Length 10579;
Best Local Similarity 100.0%; Pred. No. 5.2e-10C;
Matches 601; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2652 GGTGACAGAGCTGTCAGAGCAGGTGCTGCGAGATGGGGAAGGACTGCAGTCACTTCCGCCA 2711
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Qy   2712 GGCTGTGCAGCTTGCCTGGCGCCCCACAGGGAGGGTCCGTGCCCTCGGGACATCGGGAGA 2771
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8446 GGCTGTGCAGCT-GTCCTGGCGCCCCACAGGGAGGGTCCGTGCCCTCGGGACATCGGGAGA 8505

Qy   2772 GGGGCCGTGCCCAGCCAGCCACCTCCGGGCTTCTGCAGCCTCTGTGTGTGGACTGGGGC 2831
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8506 GGGGCCGTGCCCAGCCAGCCACCTCCGGGCTTCTGCAGCCTCTGTGTGTGGACTGGGGGC 8565

Qy   2832 ATCCTCCTACTGCCTGCCAGCCCCAGCTGGCTCTGTCTTGAGTGGGACTTGGCCCCACCC 2891
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Db   8566 ATCCTCCTACTGCCTGCCAGCCCCAGCC-GGCTCTGTCTTGAGTGGGACTTGGCCCCACCC 8625

Qy   2892 TCGTCCGGGGCCCTCCTCCCCTCATGGCACCCCTGGCCCTGGGGGTCCCCAGCGTCTCAGAG 2951
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Db   8626 TCGTCCGGGGCCCTCCTCCCCTCATGGCACCCCTGGCCCTGGGGGTCCCCAGCGTCTCAGAG 8685

Qy   2952 CTCCCCCTGCCTGCCTGAGCCACCAGCTTTCTGACCTCCACCTCAGACGCCCCTGC 3011
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Db   8686 CTCCCCCTGCCTGCCTGAGCCACCAGCTTTCTGACCTCCACCTCAGACTCAGAGCCCCTGC 8745

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Qy   3132 CCCACCAGGGTCAGGGGGGCCTGGCCTGGGGGCCTGCCCTGCCTGGGACCCCACAGCCTGAGATGTGCT 3191
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Qy   3192 TATTGGCTGCCATGGCTCTGGCACAGTCCAGTGGACCCCAGGAAGGCACAGGGTCTG 3251
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Qy   3252 A 3252
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Db   8986 A 8986

RESULT 14
AAK70045
ID   AAK70045 standard; DNA; 10579 BP.
XX
AC   AAK70045;
XX
DT   06-NOV-2001 (first entry)
XX
DE   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24857.
XX
KW   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW   cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS   Homo sapiens.
XX
PN   WO20015718.2-A2.
XX
PD   09-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01354.
XX
PR   31-JAN-2000; 2000US-0179065.
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PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0250016.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
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PR 08-DEC-2000; 2000US-0251989.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
PT Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Disclosure; SEQ ID NO 24857; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 10579 BP; 2298 A; 2894 C; 3129 G; 2258 T; 0 other;

Query Match   18.5%; Score 601; DB 22; Length 10579;
Best Local Similarity   100.0%; Pred. No. 5.2e-100;
Matches   601; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   2652 GGTGACAGAGCTGTCAGAGCAGTGCTGCAGATGCGGAAGGACTGCAGTCACTTCGCCA 2711
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   8386 GGTGACAGAGCTGTCAGAGCAGTGCTGCAGATGCGGAAGGACTGCAGTCACTTCGCCA 8445

Qy   2712 GGCTGTGCAGCTTGTCCTGCGCCCCACAGGGAGGGTCCGTGCCCTCGGGCATCGGGAGA 2771
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Db   8446 GGCTGTGCAGCTTGTCCTGCGCCCCACAGGGAGGGTCCGTGCCCTCGGGCATCGGGAGA 8505

Qy   2772 GGGGCCGTGCCCAGCCAGCCACCTCCGGGCTTCTGCAGCCTCGTGTGTGGACACTGGGGC 2831
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db    8506 GGGGCCGTGCCCAGCCAGCACCTCCGGGCTTCTCCGCAGCCTTCTGTGTGTGGGACACTGGGGC 8565

Qy    2832 ATCCTCCTACTGCCTGCAGCCCCCAGCTGGCTCTCTCTTGAGTGGGACTTGGCCCCACCC 2891
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    8566 ATCCTCCTACTGCCTGCAGCCCCCAGCTGGCTCTGTCTTGAGTGGGACTTGGCCCCACCC 8625

Qy    2892 TCGTCCGGGGCCTCCTCCCCTCATGGCACCCTGGCCCTGGGGTCCCCAGCCGTCTCAGAG 2951
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Db    8626 TCGTCCGGGGCCTCCTCCCCTCATGGCACCCTGGCCCTGGGGTCCCCAGCCGTCTCAGAG 8685

Qy    2952 CTCCCCTGGCCTCGAGCCACAGCTTTCTGGACTCAGCCGCCCCTGC 3011
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Db    8686 CTCCCCTGGCCTCGAGCCACAGCTTTCTGGACTCCACCTCAGCCGCCCCCTGC 8745

Qy    3012 CTCAGGAGACCTCTGCTCTGAGCCCAGCACCCTGCCTCCCTCCTTCTGAGGAAGG 3071
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Qy    3132 CCCACCAGGGTCAGGGGGCCTGGCCTTGCCCTGGGACCCCACAGCCTGAGGATGGTGC 3191
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Qy    3192 TATTGGCTGCCATGGCTCTGGCACAGTCAGTCAGTGGCACAGGAGGCACAGGGGTCTG 3251
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Db    8926 TATTGGCTGCCATGGCTCTGGCACAGTCCAGTGACCCAGGAAGAGGCACAGGGGTCTG 8985

Qy    3252 A 3252
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RESULT 15
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ID   ABA20015 standard; DNA; 28995 BP.
XX
AC   ABA20015;
XX
DT   23-JAN-2002 (first entry)
XX
DE   Human nervous system related polynucleotide SEQ ID NO 12345.
XX
KW   Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW   immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW   antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
KW   antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW   antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW   antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS   Homo sapiens.
XX
PN   WO200159063-A2.
XX
PD   16-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01334.
XX
PR   31-JAN-2000; 2000US-0179065.
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PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   18-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
PR   07-JUN-2000; 2000US-0209467.
PR   28-JUN-2000; 2000US-0214886.
PR   30-JUN-2000; 2000US-0215135.
PR   07-JUL-2000; 2000US-0216647.

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PR   05-JAN-2001; 2001US-0259678.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA.  Barash SC.  Ruben SM;
XX
DR   WPI; 2001-541565/60.
XX
PT   Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT   useful for preventing, diagnosing and/or treating nervous system
PT   cancers and metastases -
XX
PS   Disclosure; SEQ ID NO 12346; 1701pp - Sequence Listing; English.
XX
CC   The invention relates to novel genes (ABA11004-ABA21534) and proteins
CC   (ABB14678-ABB18001) useful for preventing, treating or ameliorating
CC   medical conditions e.g. by protein or gene therapy. The genes are
CC   isolated from a range of human tissues disclosed in the specification.
CC   The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC   in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC   and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC   marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC   (b) immune disorders e.g. Addison's disease, allergies, autoimmune
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CC   haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC   disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC   colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC   (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC   epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC   and parasitic infections.
CC   Note:The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 28995 BP; 6151 A; 8327 C; 8051 G; 6466 T; 0 other;

Query Match             18.5%;  Score 601;  DB 22;  Length 28995;
Best Local Similarity   100.0%;  Pred. No. 5.8e-100;
Matches  601;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      2652 GGTGACAGAGCTGTCAGAGCAGGTCCTGCAGATGCGGAAGGACTGCAGTCACTTCGCCA 2711
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Qy      3252 A 3252
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Db     18806 A 18806

Search completed: October  1, 2003, 16:22:13
Job time : 810 secs
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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    October  1, 2003, 15:57:40 ; Search time 211 Seconds
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                                         6802.739 Million cell updates/sec

Title:          US-09-965-830-1_COPY_6_3257
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Sequence:       1 atgccggccatgcgggcct.........aagaaggcacaggggtctga 3252

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       569978 seqs, 22091566 residues

Total number of hits satisfying chosen parameters:    1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES
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2	3245.8	99.8	3249	4	US-09-343-494-2	Sequence 2, Appli
3	3218	99.0	3857	4	US-09-336-643A-19	Sequence 19, Appli
4	3156	97.0	3355	4	US-09-358-383C-1	Sequence 1, Appli
5	3153	97.0	3249	4	US-09-358-383C-3	Sequence 3, Appli
6	2664.8	81.9	3715	4	US-09-600-776-9	Sequence 9, Appli
7	884.8	27.2	3064	4	US-09-600-776-5	Sequence 5, Appli
8	869.8	26.7	3736	4	US-09-600-776-10	Sequence 10, Appli
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11	761.2	23.4	3321	4	US-09-358-383C-17	Sequence 17, Appli
12	761.2	23.4	5107	4	US-09-358-383C-15	Sequence 15, Appli
13	572.8	17.6	1626	4	US-09-358-383C-6	Sequence 6, Appli
14	572.8	17.6	2694	4	US-09-358-383C-4	Sequence 4, Appli
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                            ALIGNMENTS

RESULT 1
US-09-600-776-1
; Sequence 1, Application US/09600776
; Patent No. 6326168
; GENERAL INFORMATION:
;  APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION:  A novel potassium channel protein
;  FILE REFERENCE: Y9903-PCT
;  CURRENT APPLICATION NUMBER: US/09/600,776
;  CURRENT FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: JP P1998-011434
;  PRIOR FILING DATE: 1998-01-23
;  PRIOR APPLICATION NUMBER: JP P1998-346198
;  PRIOR FILING DATE: 1998-12-04
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;  LENGTH: 3323
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (6)..(3257)
US-09-600-776-1

  Query Match             100.0%;  Score 3252;  DB 4;  Length 3323;
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  Matches 3252;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy   2821  GACACTGGGGCATCCTCCTACTGCTGCAGCCCCAGCTGGCTCTGTGTCTTGAGTGGGACT   2880
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Db   2826  GACACTGGGGCATCCTCCTACTGCTGCAGCCCCAGCTGGCTCTGTGTCTTGAGTGGGACT   2885

Qy   2881  TGGCCCCACCCTCGTCCGGGGCCCTCCTCCCTCGGGGCCACCTGAGCACCCGGGTCCCCCA   2940
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2886  TGGCCCCACCCTCGTCCGGGGCCCTCCTCCCTCGGGGCCACCTGAGCACCCGGGTCCCCCA   2945

Qy   2941  GGGCTCTCAGAGCTCCCCCTCGGCCCCGCAGAGCTTTCTGGACACCTCCACCTCAGACTCA   3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2946  GGGCTCTCAGAGCTCCCCCTCGGCCCCGCAGAGCTTTCTGGACACCTCCACCTCAGACTCA   3005

Qy   3001  GAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCCAGCACCCCTCCCCTCCTCCT   3060
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3006  GAGCCCCCTGCCTCAGGAGACCTCTGCTCTGAGCCCAGCACCCCTCCCCTCCTCCT   3065

Qy   3061  TCTGAGGAAGGGCTAGACTGGCCCCGCAGAGCTGGCCCGCAGAGCTGTGACCAGCTGAGGCTACCAGC   3120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3066  TCTGAGGAAGGGCTAGACTGGCCCCGCAGAGCTGTGACCAGCTGAGGCTACCAGC   3125

Qy   3121  ACTGGAGAGCGCCCCACCAGGGTCAGGGGGCCTTGCCCTGGGGACCCCACAGCCTG   3180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3126  ACTGGAGAGCGCCCCACCAGGGTCAGGGGGCCTTGCCCTGGGGACCCCACAGCCCG   3185

Qy   3181  GAGATGTGCTTATTGGCTGCCATGGCTTCTGGCACAGTCCAGTGGACCAGGAAGAGGC   3240
           ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   3186  GAGATGTGCTTATTGGCTGCCATGGCTTCTGGCACAGTCCAGTGGACCAGGAAGAGGC   3245

Qy   3241  ACAGGGGTCTGA   3252
           ||||||||||||
Db   3245  ACAGGGGTCTGA   3257
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RESULT 2
US-09-343-494-2
; Sequence 2, Application US/09343494
; Patent No. 6413741
; GENERAL INFORMATION:
;   APPLICANT: Jegla, Timothy J.
;   APPLICANT: Wickenden, Alan
;   APPLICANT: ICAgen, Incorporated
;   TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit
;   FILE REFERENCE: 018512-001320US
;   CURRENT APPLICATION NUMBER: US/09/343,494
;   CURRENT FILING DATE: 1999-05-30
;   EARLIER APPLICATION NUMBER: US 60/091,469
;   EARLIER FILING DATE: 1998-07-01
;   EARLIER APPLICATION NUMBER: US 60/116,621
;   EARLIER FILING DATE: 1999-01-21
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

; LENGTH: 3249
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3249)
;   OTHER INFORMATION: hElk
US-09-343-494-2

Query Match   99.8%; Score 3245.8; DB 4; Length 3249;
Best Local Similarity   99.9%; Pred. No. 0;
  Matches 3247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy     1  ATGCCGGCCATGGGGGCCTCCTGGCGCGCTCAGAACACCTTCCTGCACCATCGCTACG    60
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Db     1  ATGCCGGCCATGGGGGCCTCCTGGCGCGCTCAGAACACCTTCCTGCACCATCGCTACG    60

Qy    61  CGCTTCGACGGCACGCACAGTAACTTCGTCTGGCAACGCCCAGGTGGCGGGGCTCTTC   120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  CGCTTCGACGGCACGCACAGTAACTTCGTCTGGCAACGCCCAGGTGGCGGGGCTCTTC   120

Qy   121  CCGTGGTCTACTGCTCTGTGACCTGCTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC   180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  CCGTGGTCTACTGCTCTGTGACCTGCTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC   180

Qy   181  ATGCAGCGGGGCTGTGCCTGCTCCTTATGGGCCAGACACCAGTGAGCTGCTGATCCTGTAC   240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ATGCAGCGGGGCTGTGCCTGCTCCTTATGGGCCAGACACCAGTGAGCTGCTGATCCTGTAC   240

Qy   241  CAACAGATCCGCAAGGCCCTGGACGAGCACAAGAGGAGTCAAGGCTCAAGGCTGATCCTGTAC   300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  CAACAGATCCGCAAGGCCCTGGACGAGCACAAGAGGAGTCAAGGCTCAAGGCTGATCCTGTAC   300

Qy   301  CGGAAGAGCGGGGCTCCGTTCGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA   360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CGGAAGAGCGGGGCTCCGTTCGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA   360

Qy   361  GGGGAGGTGGCTCTTCTTCACAAGGACATCGCGAAACCAAGAACCGAGGG   420
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  GGGGAGGTGGCTCTTCTTCACAAGGACATCGCGAAACCAAGAACCGAGGG   420

Qy   421  GGCCCCGACAGATGGAAGGAACAGGTGGTGGCCGGCGCCGGCCGATATGGCCGGCGCCGACGATCC   480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  GGCCCCGACAGATGGAAGGAACAGGTGGTGGCCGGCGCCGGCCGATATGGCCGGCGCCGACGATCC   480

Qy   481  AAAGGCTTCAAATGCCAACCGGCTGGGCGAGCCCGTGCTCTCCACCGTCTCGGGGCAC   540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  AAAGGCTTCAAATGCCAACCGGCTGGGCGAGCCCGTGCTCTCCACCGTCTCGGGGCAC   540

Qy   541  CTGCAGAAGCAGCCCAAGGCAAGCACAAGCTCAA-AAGGGGGTGTTTGGGGAGAAACCA   600
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   542  CTGCAGAAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGGTGTTTGGGGAGAAACCA   600

Qy   601  AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCCCCTTCATCCTGTTGCACTGT   660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCCCCTTCATCCTGTTGCACTGT   660

Qy   661  GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTCGCCACACTCTATGTGGCTGTC   720
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   661  GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTCGCCACACTCTATGTGGCTGTC   720

Qy   721  ACTGTGCCCTACAGCGTGTGTGAGCACGACACGGAGCCCAGTGCCCCGCGGCCCG   780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  ACTGTGCCCTACAGCGTGTGTGAGCACGACACGGAGCCCAGTGCCCCGCGGCCCG   780

Qy   781  CCCAGCGTCTGTGACCTGGAGGTCCTGCTGACCATCGTCCTTGACATTGTGTCGAATTC   840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  CCCAGCGTCTGTGACCTGGAGGTCCTGCTGACCATCGTCCTTGACATTGTGTCGAATTC   840

Qy   841  CGTACCACATCGTGTCCAAGTCGGGCCAGGTGGTGTTTGCCCCAAAGTCATTTGCCTC   900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  CGTACCACATTCGTGTCCAAGTCGGGCCAGGTGGTGTTTGCCCCAAAGTCATTTGCCTC   900
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Qy    901 CACTACGTCACCACCTGGTTCTGCTGGATGTCAGCGCAGGCCTGCGCCTTGACCTGCTA  960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACTACGTCACCACCTGGTTCTGCTGGATGTCAGCGCAGGCCTGCGCCTTGACCTGCTA  960

Qy    961 CATGCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGTGCGCCTGCTG 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CATGCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCTGCTGAAGACGTGCGCCTGCTG 1020

Qy   1021 CGCCTGCTGCTGCGCCGGCTGCTTCCGCGGCTGGACCGGTACACGCGCCGTGGTGCTG  1080
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   1021 CGCCTGCTGCTGCGCCGGCTGCTTCCGCGGCTGGACCGGTACACGCGCCGTGGTGCTG  1080

Qy   1081 ACACTGCTCATGGGCCGTGTTCGCCGTCGGCTCCGCACTGGGTCGCCTGCGTCTGGTTTAC 1140
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Db   1081 ACACTGCTCATGGGCCGTGTTCGCCGTCGGCTCCGCACTGGGTCGCCTGCGTCTGGTTTAC 1140

Qy   1141 ATTGGCCAGCGGGAGATCGAGAGCGAATCCGAGCTGCCCTGAGATTGGCCTGCTGCAG  1200
          |||||||||||||||||||||||||||||||||||||||
Db   1141 ATTGGCCAGCGGGGAGATCGAGAGCGAATCGGAGATTGGCCTGCTGGAGG  1200

Qy   1201 GAGCTGGCCGCCGCCGACTGGAGACTCCTACTACCTGTGTGGGCCGGAGGCCAGCTGGAGGG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GAGCTGGCCGCCGCCGACTGGAGACTCCTACTACCTGTGGGCCCGGAGGCCAGCTGGAGGG 1260

Qy   1261 AACAGCCCGGCCAGAGTGACAACTGCAGCAGCAGGGACGGGCCG  1320
          ||||||||||||||||||||||||||||||||||
Db   1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGGGACGGGCTG 1320

Qy   1321 GAGGTGCTGGGGCGGGCCGTGCCCTGCACCTCCCTCTACTTCGGCANTC  1380
          |||||||||||||||||||||||||||||||||||
Db   1321 GAGGTGCTGGGGCGGGCCGTGCCCTGCACCTCCCTCTACTTCGGCACTC 1380

Qy   1381 AGCAGCCTCACCAGGTGGCGCTTCGGCAACGTGTCCGCCAACACGGACACCGAGAAGATC 1440
          ||||||||||||||||||||||||||||||||||||
Db   1381 AGCAGCCTCACCAGGTGGCGCTTCGGCAACGTGTCGGCCAACACGGACACCGAGAGAAGATC 1440

Qy   1441 TTCTTCCAGTCTGCACCATGCTCATCGGCGCCCTGATGCGCGTGGTTTGGGAAGTTG 1500
          ||||||||||||||||||||||||||||||||||||
Db   1441 TTCTTCCAGTCTGCACCATGCTCATCGGCGCCCTGATGCGCGTGGTGTTTGGGAACGTG 1500

Qy   1501 ACGGCCATCATCCAGCGCATGCCAGCGCATGGTACGGCCGCCGTTTCTGTACCGCGGAC 1560
          ||||||||||||||||||||||||||||||||||||||||||
Db   1501 ACGGCCATCATCCAGCCGCATGCCAGCCCGCATGGTACGGCCGCCGTTTCTGTACCACCAGCGCGAC 1560

Qy   1561 CTGCGGGACTACATCCGCATCCCCAAGGCCCCTCAAGCAGCCCATCTGGGAG  1620
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Db   1561 CTGCGGGACTACATCCGCATCCCCAAGGCCCCTCAAGCAGCCCATCTGGGAG 1620

Qy   1621 TACTTCGGCAGGTGCATGGGCCGTGAACAATGGCCATCGGCGACACCGCTGCTGCAGAGC 1680
          |||||||||||||||||||||||||||||||||
Db   1621 TACTTCGGCAGGTGCATGGGCCGTGAACAATGGCCATCGGCGACACCGCTGCTGCAGAGC 1680

Qy   1681 CTCCCTGACGAGCTGGGCCGTGCCCCAGCGCATCGGCACCACCAAGGAGGTCCTGCAGAGC 1740
          ||||||||||||||||||||||||||||||||
Db   1681 CTCCCTGACGAGCTGGGCCGTGCCCCAGCGCATCGGCACCACCAAGGAGGTCCTGCAGAGC 1740

Qy   1741 CCACTGTTTGAGGCGGCCAGCCTGTCTGCCCTGCGCCCC  1800
          ||||||||||||||||||||||||||||||||||
Db   1741 CCACTGTTTGAGGCGGCCAGCCTGTCTGCCCTGCGCCCC 1800

Qy   1801 TGGCCTTCGCACCGCGGCGAGTGACCTCATCACCATCCACCAAGGGCCCTCTAC 1860
          ||||||||||||||||||||||||||||||||||||
Db   1801 TGGCCTTCGCACCGCGGCGAGTGACCTCATCACCATCCACCAAGGGCCCTCTAC 1860

Qy   1861 TTTGTCTGCTCTGGCTCCATGGAGGTCTCATGGAGGTGCTCAAGGTGCTGCCACCTGTCTGCCATCCTAGGG 1920
          ||||||||||||||||||||||||||||||||
Db   1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGCTGCCACCTGTCTGCCTCTCCATCCTAGGG 1920

Qy   1921 AAGGGCGGACCTGATCGGCTGTGAGCTGCGCGGCGGAGCAGTGGTAAAGGCCAATGCC 1980
          ||||||||||||||||||||||||||||||||||||
Db   1921 AAGGGCCGACCTGATCGGCTGTGAGCTGCGCGGCGGAGCAGTGGTAAAGGCCAATGCC 1980

Qy   1981 GACGTGAAGGGCTGACGTACCTGCAGTGTCTGCAGCGCGGCTGGCCTGCACGAC 2040
          ||||||||||||||||||||||||||||||||||||
Db   1981 GACGTGAAGGGCTGACGTACCTGCAGTGTCTGCAGCGCGGCTGGCCTGCACGAC 2040
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Qy   1981 GACGTGAAGGGCTGACGTACCTGCAGTGTCTGCAGCGCGGCTGGCCTGCACGAC 2040
          ||||||||||||||||||||||||||||||||||||
Db   1981 GACGTGAAGGGCTGACGTACCTGCAGTGTCTGCAGCGCGGCTGGCCTGCACGAC 2040

Qy   2041 AGCCTTGGCCTGTACCCCGAGTTGCCCGCCCGCTTCAGTGTGTGGCCTCGAGGGGAGCTC 2100
          ||||||||||||||||||||||||||||||||
Db   2041 AGCCTTGGCCTGTACCCCGAGTTGCCCGCCCGCTTCAGTGTGTGGCCTCGAGGGGAGCTC 2100

Qy   2101 AGCTACAACCTGGGTGCTGCCTGCAGAGGTGGACACCAGCTCCCTGAGCGGC 2160
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Db   2101 AGCTACAACCTGGGTGCTGCCTGCAGAGGTGGACACCAGCTCCCTGAGCGGC 2160

Qy   2161 GACAATACCCTTATGTCCACGCTGGAGGAGGACACAGATGGGGAGCAGGGCCCCACC 2220
          ||||||||||||||||||||||||||||||||||||
Db   2161 GACAATACCCTTATGTCCACGCTGGAGGAGGACACAGATGGGGAGCAGGGCCCCACG 2220

Qy   2221 GTCTCCCCAGCCCAGCTGATGAGCCTCCAGCCCCGTGTTGTCCCCTGCCACCTCC 2280
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Db   2221 GTCTCCCCAGCCCAGCTGATGAGCCTCCAGCCCCGTGTTCCCGCCCTGGCTGCACCTCC 2280

Qy   2281 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGCGTGAGGCTTGAAGGCTGCTCGTCTAGGT 2340
          ||||||||||||||||||||||||||||||||
Db   2281 TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTGCTATCCCCACGTCGAACAGCGTGAGGCTTGAAGGCTGCTCGTCTAGGT 2340

Qy   2341 GGCAGAGGGAGGCCCAGGCCAGGCCTTGAAGGCTTGAAGGCTGCCCCCCTGCTCCC 2400
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Db   2341 GGCAGAGGGAGGCCCAGGCCAGGCCTTGAAGGCTTGAAGGCTGGCCCCCTGCTCCC 2400

Qy   2401 CCACGGGCCCTAGAGGGGCTACGGCTGCCCCATGCCATGGAATGTGCCCCCAGATCTG 2460
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Db   2401 CCACGGGCCCTAGAGGGGCTACGGCTGCCCCATGCCATGGAATGTGCCCCCAGATCTG 2460

Qy   2461 AGCCCCAGGGTAGTAGATGCATTGAAGACGGGCTGTGGCTGGCCAGCCAAGTTCTCT 2520
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Db   2461 AGCCCCAGGGTAGTAGATGCATTGAAGACGGGCTGTGGCTGGCCAGCCAAGTTCTCT 2520

Qy   2521 TTCGGGCTGGGCCAGTCGTGCGCCGGAATGTAGCGCAGAGCCCCTCCCCGACCAGAGCC 2580
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Db   2521 TTCGGCGTGGGCCAGTCGTGCCGGAATGTAGCGCAGAGCCCCTCCCCGACCAGAGAGC 2580

Qy   2581 GGCTGCTCACTGTTCCCCATGGCCCCAGGCGGCAAGGAACACACTGGACAAG 2640
          ||||||||||||||||||||||||||||||||
Db   2581 GGCCTGCTCACGTGTTCCCCATGGCCCCAGGCGGCAAGGAACACACTGGACAAG 2640

Qy   2641 CTTCGGCAGGCGGTGACAGAGCGTGTCAGAGCAGGTGCTGCAGAGGTGGAAGACTGCAG 2700
          ||||||||||||||||||||||||||||||||
Db   2641 CTTCGGCAGGCGGTGACAGAGCGTGTCAGAGCAGGTGCTGCAGAGGCGGAAGACTGCAG 2700

Qy   2701 TCACTTCGGCTGTGTCAGCTGTGCCCAGCTGCTTCTGCGGCCTCCCTCGG 2760
          ||||||||||||||||||||||||||||||||
Db   2701 TCACTTCGGCTGTGTCAGCTGTGCCCAGCTGCTTCTGCGGCCTCCCTCGG 2760

Qy   2761 GCATCGGGGAGAGGGGCATCCTCTACTGCCTGCCCAGCCTGCTCTGCTTCTTGAGTGGGACT 2820
          ||||||||||||||||||||||||||||||||
Db   2761 GCATCGGGGAGAGGGGCATCCTCTACTGCCTGCCCAGCCTGCTCTGCTTCTTGAGTGGGACT 2820

Qy   2821 GACACTGGGGCATCCTCCAGCCCCCAGCTGCTCTCGGCCCCCCAGCTGTCTGCTGGGTCCCCCA 2880
          ||||||||||||||||||||||||||||||||
Db   2821 GACACTGGGGCATCCTCCAGCCCCCAGCTGTCTGCTGGGTCCCCCA 2880

Qy   2881 TGGCCCCACCCGTCCGGGCCTCCCCCTCATGGCACCCCCTGGGGTCCCCCA 2940
          ||||||||||||||||||||||||||||||||
Db   2881 TGGCCCCACCCGTCCGGGCCTCCCCCTCATGGCACCCCCTGGGGTCCCCCA 2940

Qy   2941 GGGTCTCAGAGCTCCCCCTGGCCTCGGCCACCAGCTTCTGGACCTTCACCTCAGACTCA 3000
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Db   2941 GGCTCTCAGAGCTCCCCCTGGCCTCTGGCCACCAGCTTCTGGACCTTCACCTCAGACTCA 3000

Qy   3001 GAGCCCCTGCCTCGCCCCTCAGGAGGACCTCGCTGCTGCTCTGCTCCCTCCT 3060
          ||||||||||||||||||||||||||||||||
Db   3001 GAGCCCCTGCCTCGCTCCCTCAGGAGGACCTCGCTGCTGCTCTGCTCCCTCCT 3060

Qy   3061 TCTGAGGAAGGGGCTAGGGGCTGAGCTGGGCCGCGAGTTGGGCCGCGAGTGAGGCTACCAGC 3120
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Db  3061  TCTGAGGAAGGGGCTAGGACTGGGCCCGCAGAGCCTGTGAGCCAGGCTGAGGCTACCAGC  3120
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Qy  3121  ACTGGAGGAGCCCCCACCAGGGTCAGGGGGGCTGGCCTTGCCCTGGGACCCCACAGCCGG  3180
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Db  3121  ACTGGAGAGCCCCCACCAGGGTCAGGGGGGCTGGCCTTGCCCTGGGACCCCACAGCCTG  3180

Qy  3181  GAGATGTGCTTATTGGCTGCCACAGTCTCTCGGCACAGTGGTGGCCGATATGGCGGGCACGATCC  3240
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Db  3181  GAGATGTGCTTATTGGCTGCCCATGGCTCTCGGCACAGTCCAGTGGCACGATGGCGGGCACGATCC  3240

Qy  3241  ACAGGGGTC  3249
                |||||||||
Db  3241  ACAGGGGTC  3249


RESULT 3
US-09-336-643A-19
; Sequence 19, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
;  APPLICANT: Miller, Andrew P.
;  APPLICANT: Curran, Mark Edward
;  APPLICANT: Hu, Ping
;  APPLICANT: Rutter, Marc
;  APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/115,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;  LENGTH: 3857
;  TYPE: DNA
;  ORGANISM: H. sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (249)...(3495)
;  OTHER INFORMATION: K+Hnov14
US-09-336-643A-19

Query Match         99.0%;  Score 3218;  DB 4;  Length 3857;
Best Local Similarity  99.8%;  Pred. No. 0;
Matches 3244:  Conservative  0;  Mismatches  5;  Indels  3;  Gaps  2;

Qy    1  ATGCCGGCCATGCGGGGCCTCCTGCGCCTCAGAACACCTTCCTGGACACCGCTACG  60
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Db  249  ATGCCGGCCATGCGGGGGCCTCCTGCGCCTCCGCCCCAGAACACACTTCCTGGACACCGCTACG  308

Qy   61  CGCTTCGACGGCACGCACGCACAGTAACTCGTCGTCTGGCAACGCCCCAGTGCGGGGCTCTTC  120
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Db  309  CGCTTCGACGGCACGCACGCACAGTAACTCGTCGTCTGGCAACGCC--AGTGCGGGGCTCCT-  365

Qy  121  CCCGTGGTCTACTGCTTCTGTGATGGCTTCTGTGTGACCTTCACGGGCTTCTCCCGGCTGAGTC  180
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Db  366  CCCGTGGTCTACTGCTTCTGTGATGGCTTCTGTGTGACCTTCACGGGCTTCTCCCGGCTGAGTC  425

Qy  181  ATGCAGCGGGGGCTGTGCCAAGGCCCCGGACAGCAGCAAGGAGTTCAAGGTCGTGAGTC  240
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  426  ATGCAGCGGGGGCTGTGCCAAGGCCCCGCAGAACACCAGTCGTGAGCTCGTGAGTC  485

Qy  241  CAACAGATCCGCAAGGCCC-GGACAGCACAAGGAGTTCAAGGAGTTCAAGGCTGTGTAC  300
             ||||||||||||||||||  ||||||||||||||| ||||||||||||||| |||||
Db  486  CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGAGTTGATCCTGTAC  545

Qy  301  CGGAAGAGCGGGGGCTTCCCGTTCTCTGGTGTCCTGGATGTGATTACCCATAAAGAATGAGAAA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  CGGAAGAGCGGGGGCTTCCCGTTCTCTGGTGTCCTGGATGTGATACCCATAAAGAATGAGAAA  360
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Db  546  CGGAAGAGCGGGGGCTCCCGTTCTGTGTCTTCCTGGATGTGATACCCATAAAGAATGAGAAA  605
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Qy  361  GGGGAGGTGGCTCTCTTCCTCCTCAGTCTCTCACAAGGACATCAGCAGGAAACCAAGCCGGG  420
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  606  GGGGAGGTGGCTCTCTTCCTCCTCAGTCTCTCACAAGGACATCAGCAGGAAACCAAGCCGGG  665

Qy  421  GGCCCCGACAGATGGAAGGAGACAGTGGTGGCCGGCGCCGATATGGCGGGCACGATCC  480
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Db  666  GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGCGCCGGCCGATATGGCGGGCACGATCC  725

Qy  481  AAAGGCTTCAATGCCAACCTGGCCTACCACCTGTCCGGGCAC  540
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Db  726  AAAGGCTTCAATGCCAACCTGCCCTCCTACCACCTGTCCGGGCAC  785

Qy  541  CTGCAGAAGCAGCCAAGGCAAGCACAGCTCAATAAGGGGTGTTTGGGGAGAAACCA  600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  786  CTGCAGAAGCAGCCAGCCCAAGGCAAGCACAGCTCAATAAGGGGTGTTTGGGGAGAAACCA  845

Qy  601  AACTTGCCTGAGTACAAAGTAGCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT  660
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Db  846  AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT  905

Qy  661  GGGGCACTGAGAGCCACCTGGATGGCTTCATCCTGCTCGGCCACACTCTATGTGGCGTC  720
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  906  GGGGCACTGAGAGCCACCTGGATGGCTTCATCCTGCTCGGCCACACTCTATGTGGCGTC  965

Qy  721  ACTGTGCCTACAGCGTGTGTGAGCACAGCAGCGGGGAGCCCGGCGCCGCCG  780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  966  ACTGTGCCTACAGCGTGTGTGAGCACAGCAGCGGGGAGCCCCGGCGCCGCCG  1025

Qy  781  CCCAGGTCTGTGACCTGGCGTGGAGTCCTCTTCATCCTGACATTGTGCTGAATTC  840
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db  1026  CCCAGGTCTGTGACCTGGCGTGGAGTCCTCTTCATCCTGACATTGTGC-GAATTC  1085

Qy  841  CGTACCACATTCGTCCAAGTGCGGGTCGCCAGGTGGTGTTCCCCAAAGTCCATTTGCCTC  900
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1086  CGTACCACATTCGTCCAAGTGCGGGTCGGCCAGGTGGTGTTCCCCAAAGTCCATTTGCCTC  1145

Qy  901  CACTACGTCACCACCTGGTCTCCTGCTGCAGGCTGCCCTTTGACCTGCTA  960
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1146  CACTACGTCACCACCTGGTCTCCTGCTGCAGGCTGCCCTTTGACCTGCTA  1205

Qy  961  CATGCCCTTCAAGGTCAACCTGTACTTCGGGGCCCATCCTGTGAAGACGTGCGCCTGTG  1020
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1206  CATGCCCTTCAAGGTCAACCTGTACTTCGGGGCCCATCCTGTGAAGACGTGCGCCTGTG  1265

Qy  1021  CGCCTGCTGCGCCCTGCTTCCGGCACTGGCTCGCTGGCCGCTACCGTCGCAGTACAGCACCCTGTCG  1080
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1266  CGCCTGCTGCGCCCTGCTTCCGGCACTGGCTGCGCTGGCCGCTACCGGTCGCAGTACAGCACCCTGTCG  1325

Qy  1081  ACAGCTGCTCATGGCCGTGTCGCCCTGCCGCTGGGTCGCCGCTGGCCGCTGGTTTAC  1140
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  1326  ACAGCTGCTCATGGCCGTGTTGCCCTGCCGCTGGGTCGCCGCTGGCCGCTGGTTTAC  1385

Qy  1141  ATTGGCCAGCGGGGAGATCGGGGAGCAGCGAATCCGAGCAGCAGCGGCTCTTC  1200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1386  ATTGGCCAGCGGGGAGATCGGGGAGCAGCGAATCCGAGCAGCAGCGGCTCAG  1445

Qy  1201  GAGCTGGCCGCCCGCCGGACTCCTGAGACTCCTACTGGTGGGGCCAGCGGAGGG  1260
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Db  1446  GAGCTGGCCGCCCGCCGGACTCCTACTGGTGGGGCCAGCAGCTGGAGGG  1505

Qy  1261  AACAGCTCCGGCAGAGTGACAACTGCAGCAGCGAGGCAACGGGCGGCTG  1320
              |||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1321  GAGCTGTGGGCGGGCCCGTCGCCGGCACCGGCTGGCTGCCTACACCTTCGCACTC  1380
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Db  1566  GAGCTGTGCTGGGCGGGCCCGTCGCCGGCAGCGGCTGCCTACACCACCTTCGCACTC  1625

Qy  1381  AGCAGCCTCACCAGCTGTCCGGCAACGTGTCCGCAACACCGAGAGATC  1440
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Qy   2521 TTCCGGCGTGGGCCAGTCTGGCCGTGGAATGTAGCAGCGCCCCTCCCTGACCAGAGAGC 2580
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Qy   2581 GGCCTGCTCACTGTTCCCATGGGCCCAGGGACCAAGGAACACAGAACACTGACAAG 2640
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Qy   2641 CTTCGGCAGGCGGTGACAGAGCTGTCAGAGCAGCAGTGCTGCAGATGGGGAAGGACTGCAG 2700
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Db   2886 CTTCGGCAGGCGGTGACAGAGCTGTCAGAGCAGCAGTGCTGCAGATGGGGAAGGACTGCAG 2945

Qy   2701 TCACTTCGGCAGGCTGTGCAGCTTGTCCTGCGCGCCCACAGGGAGGGGTCCGTGCCCTCGG 2760
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Db   2946 TCACTTCGGCAGGCTGTGCAGCTTGTCCTGCGCGCCCACAGGGAGGGGTCCGTGCCCTCGG 3005

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Db   3006 GCATCGGGAGAGGGGCCGTGCCCAGCCAGCAGCCACCTCCGGGCTCTGCAGCCTCTGTGTG 3065

Qy   282? GACACTGGGGCATCCTCCTACTGCCTGCAGCCCCAGCTGGCTCGTGTTCTTGAGTGGGAC? 2880
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Db   3066 GACACTGGGGCATCCTCCTACTGCCTGCAGCCCCAGCTGGCTCGTGTTCTTGAGTGGGACT 3125

Qy   2881 TGGCCCCACCCTCGTCCGGGCCTCTCCCCCATGGCACCCTGGCCCTGGGGGTCCCCA 2940
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Db   3126 TGGCCCCACCCTCGTCCGGGCCTCTCCCCCATGGCACCCTGGCCCTGGGGTCCCCA 3185

Qy   2941 GCGTCTCAGAGCTCAGAGGCTCCCCCTGGCTCGAGCCCAGCGCTTCTCTGACCTCCACCTCAGACTCA 3000
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3186 GCGTCTCAGAGCTCAGAGGCTCCCCCTGGCTCGAGCCCAGCGCTTCTCTGACCTCCACCTCAGACTCA 3245

Qy   3001 GAGCCCCTGCTCAGAGAGACCTCTGCTCTGAGCCCAGCCTCCT 3060
           ||||||||||||||||||||||||||||||||||||||||||
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Qy   3061 TCTGAGGAAGGGCTAGGACTGGGCCCCGCCAGGCCTGAGCGAGGCTACCAGC 3120
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Db   3306 TCTGAGGAAGGGCTAGGACTGGGCCCCGCCAGGCCTGAGCGAGGCTACCAGC 3365

Qy   3121 ACTGGAGGAGCCCCTGCTCAGGGGTCAGGGGCCTGGGACCCCAGCCTG 3180
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   3366 ACTGGAGGAGCCCCTGCTCAGGGGTCAGGGGCCTGGGACCCCAGCCTG 3425

Qy   3181 GAGATGTGCTTATTGGCTGCCATGGCTGCACAGTCCAGGGAAGAGGC 3240
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Db   3426 GAGATGTGCTTATTGGCTGCCATGGCTGCACAGTCCAGGGAAGAGGC 3485

Qy   3241 ACAGGGGTCTGA 3252
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Db   3486 ACAGGGGTCTGA 3497

Qy   1441 TTCTCCATCTGCCACCATGCTCATCGGGGCGCCCTGATGCACGCGGTGGTGTTTGGGAACGTG 1500
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Db   1686 TTCTCCATCTGCCACCATGCTCATCGGGGCCCCTGATGCACGCGGTGGTGTTTGGGAACGTG 1745

Qy   1501 ACGGCCATCATCCAGCGCATGTACGCCCGCGTTCTGTACCACAGCCCGCACGCGCGAC 1560
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Db   1746 ACGGCCATCATCCAGCGCATGTACGCCCGCGTTCTGTACCACAGCCCGCACGCGCGAC 1805

Qy   1561 CTGCGCGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCAGGCATGCTGGAG 1620
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Db   1806 CAGCGCGACTACATCCGCATCCACCGTATCCCCAAGCCCTCAAGCAGCAGGCATGCTGGAG 1865

Qy   1621 TACTTCCAGGCACCTGGGCGGTGAACAATGGCGTGACCACCACCGAGCTGCTGCAGAGC 1680
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Qy   1681 CTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCCTGCAGCTG 1740
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Db   1926 CTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCCTGCAGCTG 1985

Qy   1741 CCACTGTTTGAGCGGCGCCAGCCGGCGCTGCCTCGCCGGGGACTGTCTCTGGCCCTCCGGCCC 1800
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Db   1986 CCACTGTTTGAGCGGCGCCAGCCGGCGCTGCCTCGCCGGGGCACTGTCTCTGGCCCTGCGGGCCC 2045

Qy   1801 GCCTTGCTGCACGCCGGCGAGTACTTCATCCACCAAGGCGATGCCTGGCCAGGCCCTCTAC 1860
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Db   2046 GCCTTGCTGCACGCCGGCGAGTACTTCATCCACCAAGGCGATGCCTGGCCAGGCCCTCTAC 2105

Qy   1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGCACCGTGCCGTGCTCGCCATCCTAGGG 1920
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Qy   1921 AAGGGCGACCTGATCGGCGTGTGAGCTGCCCCGGCGGAGCCAGGTTGGTAAAGGCCAATGCC 1980
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Db   2166 AAGGGCGACCTGATCGGCGTGTGAGCTGCCCCGGCGGAGCCAGGTTGGTAAAGGCCAA-GCC 2225

Qy   1981 GACGTGAAGGGGCTGACTCGTCTCGGTGTCTCAGTGGCTGCTGGCTGCGACGAC 2040
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Db   2226 GACGTGAAGGGGCTGACTCGTCTCGGTGTCTCAGTGGCTGCTGGCTGCGACGAC 2285

Qy   2041 AAGGGCGACCTGATCGGCGTACCCGAGTTGCCCCGGAGCCAGGTGCTCGTGGCCTCCAGTGGGGGAGCTC 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2286 AGGGGCTGCCTGCGTGATCGGCGTACCCGAGTTGCCCCGGAGCCAGGTGCTCGTGGCCTCCAGTGGGGGAGCTC 2345

Qy   2101 AGCTACAAACCCGGGTGCTGGGGAGGCTCGCAGAGGTGGACACCAGCTCCCTGAGCGGC 2160
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Db   2346 AGCTACAAACCCGGGTGCTGGGGAGGCTCGCAGAGGTGGACACCAGCTCCCTGAGCGGC 2405

Qy   2161 GACAAAATACCCTATGTCCACGCTGGAGGAAGGAGAACAGATGGGAGCAGGCCCCACG 2220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2406 GACAAATACCCTATGTCCACGCTGGAGGAAGGAGAACAGATGGGAGCAGGCCCCACG 2465

Qy   2221 GTCTCCCCAGCCCCAGCTGATGAGCCCTCAGCTTCCCCTGGCCTGCTGCACCTCC 2280
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Qy   2281 TCATCCTCAGTCTGCCAAGCTGCTATCCCCAACACGCACCACCTCGTCTAGGT 2340
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Db   2526 TCATCCTCAGTCTGCCAAGCTGCTATCCCCAACACGCACCACCTCGTCAGGT 2585

Qy   2341 GGCAGAGGGAGGCCAGGCCAGGGCTTGAAGGGCTGGAGGCTGAGGCTGAGGCTCCC 2400
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Db   2586 GGCAGAGGGAGGGCCAGGCCAGGGCTTGAAGGGCTTGAAGGCTGAGGCTGCCCTGCTGCCC 2645

Qy   2401 CCACGGGGCTACGGCTACGGGCTACGGCTGCCCCATGCCATGGAATCGCCCCCAGATCTG 2460
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Db   2646 CCACGGGGCCCCTAGAGGGGCTACGGCTGCCCCATGCCATGGAATGGCCCCCAGATCTG 2705

Qy   2461 AGCCCCAGGTAGTAGATGCCATTGAAGACGGCCTGTGGCTTCGGACCACCCAAGTTCTCT 2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2706 AGCCCCAGGTAGTAGATGCCATTGAAGACGGCCTGTGGCTTCGGACCACCCAAGTTCTCT 2765

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; LOCATION: (104)..(3352)
US-09-358-383C-1

Query Match      97.0%;  Score 3156;  DB 4;  Length 3355;
Best Local Similarity   98.2%;  Pred. No. 0;
Matches 3192:  Conservative  0;  Mismatches  60;  Indels  0;  Gaps  0;

Qy      1 ATGGCGGCCATGCGGGGGCCTCCTGGCCGCTTCAGAACACCTTCCTGGACACACTCGCTACG 60
            |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    104 ATGGCGGCCATGCGGGGGCCTCCTGGCCGCCGCAGAACACCTTCCTGGACACCATCGCCACG 163

Qy     61 CGGTTCGACGGCAGCAGCACAACTAACTTCGTGCTGGGCAACGCCCAGTGGCGGGGGCTCTTC 120
            |||||||||||||||| ||||||||||||||||| ||||||||||||||||||||||||
Db    164 CGGTTCGACGGCAGCAGCACAACTAACTTCGTGCTGGGCAACGCCCAGTGGCGGGGGCTCTTC 223

Qy    121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC 180
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Db    224 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC 283

Qy    181 ATGGCAGCGGGGGCTGTGCCTGCTTCCTTTATGGGCCAGACACCAGTCGTCCGC 240
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Db    284 ATGGCAGCGGGGGCTGTGCCTGCTTCCTTTATGGGCCAGACACCAGTCGTCCGC 343

Qy    241 CAACAGATCCGCAAGGCCCTGAACGAGCACAGGGTTCAAGGTCACCACCAGTCGTCCTGTAC 300
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Db    344 CAACAGATCCGCAAGGCCCTGAACGAGCACAGGGTTCAAGGTCACCACCAGTCGTCCTGTAC 403

Qy    301 CGGAAGAGGGGGCTCCCGTTCTCGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA 360
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Db    404 CGGAAGAGGGGGCTCCCGTTCTCGGTGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA 463

Qy    361 GGGGAGGTGGCTCTTCCTCCTAGTCTCCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420
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Qy    421 GGCCCCGACGAGATGGAAGGAGGACAGTGGTGCCGCGGCCGATATGGCGGGCACGATCC 480
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Qy    481 AAAGGCTTCAATGCCAACCGGCGGGCGGAGCCCGTGCTCTCACCACCGTCCGGGCAC 540
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Qy    541 CTCGCAGAAGCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGTGTTGGGAGAAACCA 600
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Db    644 CTGCAGAAGCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGTGTTGGGAGAAGCCA 703

Qy    601 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTGTTGCACTGT 660
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Db    704 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTGTTGCACTGT 763

Qy    661 GGGGGACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCCACACTCTATGTGTCGTGTC 720
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Db    764 GGGGGCGCTGAGGGCCACCTGGGATGGCTTCATCCTGCTCGCCCACACTCTATGTGTCGTGTC 823

Qy    721 ACTGTGCCCTACAGGTGTGTGACGACAGCACGGAGACACGGAGCCGCCCGCGGCCCCG 780
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Db    824 ACCGTGCCCTACAGGTGTGTGACGACAGCACGGAGACACGGAGCCGCCCGCGGCCCCA 883

Qy    781 CCCAGCGTCGTGTGAGCCGGTGGAGGTCCTCTCATCCTTGACATTGTGCCTGAATTTC 840
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Qy    841 CGTACCACAATTCGTGTCCACCTGGTGTTCCTCCAGCGTGTTCATCGGCCCAAAGTCCTC 900
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Db    944 CGTACCACAATTCGTGTCCACCTGGTGTTCCTCCAGCGTGTTCATCGGCCCAAAGTCCTC 1003

Qy    901 CACTGTTGCGTCGTCCTGTGATGTCATCGACGCCTGCCCTTGACCTGCTA 960
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Db   2021 CGCCTGCTGCGGCCTGCTCCGGGACCGGTACTCGCAGTACAGCGGCCGGTGGTCG 1183

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Qy   1141 ATTGGGCCAGGGAGATCCAGAGCAGCGAATCCGAGCTGCCTGAGATTGGGCTGGCGGCAG 1200
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Qy   1201 GAGCTGGCCGCGACTGAGACTCCCTACTACCTGGTGGGCCAGACTGGAGGG 1260
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Db   1364 AACAGCTCTGGCCAGAGTGACAACTGCAGCAGCAGCAGCGGCAGCGAGGCGGGGCTG 1423

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Qy   1381 AGCAGCCTCCACCAGCTGGCTTCGGCAACGTGCCGCCCTGATGCACGCGGTGTTTGGGAACGTG 1440
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Db   1604 ACGGCCATCATCAGCGCCATGTACGCCCGGCCGTTTCGTACCAGCGCCGACGCGCGCCAC 1663

Qy   1561 CTGCGGGACTACATACCGCATCCACCGTATCCCCAAGCAGCCCCGCATGGCTCGGGCAC 1620
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Db   1664 CTGCGGGACTACATCCGCATCCACCGTATCCCCAAGCAGCCCATCCCGAGCGGGGGCAC 1723

Qy   1621 TACTTCCAGGCCACTGGGCGGTGAACAATGGCATCGACAGCACTGGAGAGC 1680
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Db   1724 TACTTCCAGGCCACCTGGGCGGTGAACAATGGCATCGACAGCACTGGAGAGC 1783

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Db   1784 CTCCCTGACGAGGTCTGCGCGCGCCAGACACTGCACCTGCACAAGAGGTTCGCAGCTG 1843

Qy   1741 TACTTCCAGGCCACTGGGTGTTGGGGAGAAACCA 1800
            |||||||||||| ||||||| |||||||||||
Db   1844 CCGCTGTTTGAGGCCACCGGGTGTTGGGGAGAAGCCA 1903

Qy   1801 GCCTTCTGCACGCGGGCGGAGTCATCACCAAGGCGATGCCCTCAGGCCCTAC 1860
            ||| |||||||||||||||||||| |||||||| ||||||||| ||||||
Db   1904 GCCTTCTGCACGCGGGCGGAGTCATCACCAAGGCGATGCCCTCAGGCCCTAC 1963

Qy   1861 TTTGTCTGCTCTTGGCTCCATGGAGGTGCTCAAGGGTGTCGCACCGTCTCGCAGTACTAGG 1920
            ||||||||||||||||||||||||||||||||||| |||||||| |||||
Db   1964 TTTGTCTGCTCTTGGCTCCATGGAGGTGCTCAAGGGTGTCGCACCGTCTCGCAGTCCTAGG 2023

Qy   1921 AAGGGCGACCTGATCGGCTGTGAGCTGCGTACTGCTGGCAGGAGCAGGCAATGCC 1980
            |||||||||||||||||||||||||||||||||||| ||||||||||||
Db   2024 AAGGTGACCTGATCGGCTGTGAGCTGCGTACTGCTGGCAGGAGCAGGCCAACGCC 2083

Qy   1981 GACGTGAAGGGCTGACGTACGCCGAGCCTCGGCGTGTCTGCGCCTGGCCTGCTA 2040
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Db   2084 GATGTGAAGGGCTGACGTACGCCGAGCCTCGCAGCTGGCCTGCTCGCACGAC 2143

Qy   2041 AGCCTTGCGCGTGTACCCGAGTTTGCCCGCGCGTTGCCCGCGACGGTGCCGCCTGCTC 2100
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Db   2144 AGCCTTGCCTCTACCGAGTTTGCCCGCGCGTTGCCCGCGACGGTGCCGCCTGCTC 2203
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Qy   3181  GAGATGGTGCTTATTGGCTGCCATGCTCTGGCACAGTCCAGTGGACCCAGGAAGAAGGC  3240
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Qy   3241  ACAGGGGTCTGA  3252
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RESULT 5
US-09-358-383C-3
; Sequence 3, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
;   APPLICANT: Curtis, Rory A.J.
;   FILE REFERENCE: MNI-055CP
;   TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
;   CURRENT APPLICATION NUMBER: US/09/358,383C
;   CURRENT FILING DATE: 1999-07-21
;   PRIOR APPLICATION NUMBER: USSN 09/119,855
;   PRIOR FILING DATE: 1998-07-21
;   NUMBER OF SEQ ID NOS: 36
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 3249
;   TYPE: DNA
;   ORGANISM: Macaca sp.
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3249)
US-09-358-383C-3

  Query Match   97.0%; Score 3153; DB 4; Length 3249;
  Best Local Similarity   98.2%; Pred. No. 0;
  Matches 3189; Conservative   0; Mismatches   60; Indels   0; Gaps   0;

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Qy      1  ATGCCGGCCATGCGGGGCCTCCTGGGGCCTCAGAACACCTTCGTGGGCACCATCGCTACG    60
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Db      1  ATGCCGGCCATGCGGGGCCTCCTGGGGCCTCAGAACACCTTCGTGGGCACCATCGCTACG    60

Qy     61  CGCTTCGACGGCACGCACGGTAACTTCGTGCTGGCAACGCCCAGGTGGCCGGGCTCTTC   120
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Db     61  CGCTTCGACGGCACGCACGGTAACTTCGTGCTGGCAACGCCCAGGTGGCCGGGCTCTTC   120

Qy    121  CCCGTGGTCTACTGCTCTCTGATGTGCTTCTGTGACCTCGTCTCCCGGGCTTAGGTG    180
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Db    121  CCCGTGGTCTACTGCTCTCTGATGCCTCTGTGACCTCGTCTCCCGGGCTTGAGGTC    180

Qy    181  ATGCAGCGGGGCGTGTGCCTGCCTCCTTTATGGGCCAGACACCAGTGAGCTGTCCGC   240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  ATGCAGCGGGGCGTGTGCCTGCCTCCTTTATGGGCCAGACACCAGTGAGCTGTCCGC   240

Qy    241  CAACAGATCCGCAAGGCCCGAAGGCACCAAGGAGTTCAAGGCTCAGCTGATCGTGTAC   300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CAACAGATCCGCAAGGCCCGAAGGCACCAAGGAGTTCAAGGCTCAGCTGATCGTGTAC   300

Qy    301  CGGAAGAGCGGGCTCCGTTCCCGTTCTGGTGTCCTCCTGATGTGATACCCATAAAGAAATGAGAAA  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CGGAAGAGCGGGCTCCGTTCCCGTTCTGGTGTCCTCCTGATGTGATACCCATAAAGAATGAGAAA  360

Qy    361  GGGGAGGTGGCTCTCTCTTCCTAGTCTTCACAAGGACATCAGGGAAACCAAGAACCGAGGG  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GGGGAGGTGGCTCTCTCTTCCTAGTCTTCACAAGGACATCAGGGAAACCAAGAACCGAGGG  420

Qy    421  GCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGGGCCGATATGGGCCGCACGATCC   480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  GGCCCGACAGATGGAAGGAGACAGGTAGTGGCCGGGCCGATATGGGCCGCACGATCC   480

Qy    481  AAAGGCTTCAATGCCAACCGGCCGGAGGCCGTGCTGCTTACCACCTGTCCGGGCAC   540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  AAAGGCTTCAATGCCAACCGGCCGGAGGCCGTGCTGCTTACCACCTGTCCGGGCAC   540

Qy    541  CTGCAGAAGCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA   600
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Qy   2101  AGCTACAAACTGGGTGCTGGGGAGGCTCTGAGAGGTGGACACCAGCTCCCTGAGCGGGC  2160
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Db   2204  AGCTACAAACTGGGTGCTGGGGAGGCTCTGAGAGGTGGACACCAGCTCCCTGAGCGGGC  2263

Qy   2161  GACAATACCCTTATGTCCACGCTGGAGGAGGAGACAGATGGGGAGCAGGGCCCCACG  2220
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2264  GACAATACCCTTATGTCCACGCTGGAGGAGGAGACAGATGGGGAGCAGGGCCCCACA  2323

Qy   2221  GTCTCCCCAGCCCAGTCGATGAGCCCTCCAGCCCCTGCTGTCCCCTGGCTGCACCTCC  2280
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2324  GTCTCCCCAGCCCAGTCGATGAGCCCTCCAGCCCCTACTGTCCCCTGTTGCACCTCC  2383

Qy   2281  TCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGCACACCCGGCTCGTCGTAGGT  2340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2384  TCATCCTCGGCTGCCAAGCTGCTATCCCCACGTCGAACAGCACACCCGGCTCGTCGTAGGT  2443

Qy   2341  GGCAGAGGGAGGCCAGGCAGGCAGGGCTTGAAGGCTGAGGCGGGCCCCTCTGCTCCC  2400
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2444  GGCAGAGGGAGGACCAGGCAGGCAGGGCTTGAAGGCTGAGGCGGGCCCCTCTGCTCCC  2503

Qy   2401  CCACGGGCCCTAGAGGGGCTACGGCTGCCCCATGCAGGCGATGTGCCCCCAGATCTG  2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2504  CCACGGGCCCTAGAGGGGCTACGGCTGCCCCCCAGCCATGGAATGTGCCCCCAGACTG  2563

Qy   2461  AGCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGCCTGCTCCGGACCAAGTTCTCT  2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2564  AGCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTGCTCCGGACCAGCCAAGTTCTCT  2523

Qy   2521  TTCCGGCTGTGGGGCCAGTCTGGCCCGGAATGTAGCACGACAGCCCTCCTGGACCAGAGAGC  2580
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Db   2624  TTCCGGCTGTGGGGCCAGTCTGGCCCGGAATGTAGCACGACAGCCCTCCTGGACCAGAGAGT  2683

Qy   2581  GGCCTGCTCACTGTTCCCCATGGGCCCAGCCAGGCCGAGGCAAGAACACAGACACACTGGACACAAG  2640
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Db   2684  GGCCTGCTCACTGTCCCCCATGGGCCCAGCCAGGCCGAGGCAAGAACACAGACACACTGGACACAAG  2743

Qy   2641  CTTCGGCAGGCCGGTGACGAGCTGCAGAGCTGGCAGGTGCAGATGCGGAAGGACTGCAG  2700
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Db   2744  CTTCGGCAGGCCGGTGAGTGGAGCTGCAGAACAGTGCTGCAGATGCGGAAGGACTACACAG  2803

Qy   2701  TCACTTCGCCAGCCTGTCAGCTTGTGTCTGCTCCAGAGGGAGGGTCCGTGCCCTCGG  2760
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Db   2804  TCACTTCGCCAGCCTGTCAGCTTGTGTCTGCTGCAGATAGGAGGGTCCACATGCCCTCGG  2863

Qy   2761  GCATCGGGAGAGGGGCCGTGCCCAGCCAGCACCTCGGGGCTTCTCAGCCTCGTGTGTG  2820
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Db   2864  GCCTCAGGAGAGGGGCCATGCCCAGCCAGCACCTCGGGGCTTCTCAGCCTCGTGTGTG  2923

Qy   2821  GACACTGGGGCATCCTCCTACTGGCCCTGGCTCTGTCTGTGAGTGGGACT  2880
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2924  GACACTGGGGCATCCTCCTACTGGCCCTGGCTCTGTCTGTGAGTGGGACT  2983

Qy   2881  TGGCCCCACCCTGCCTGTCCTCCTCGCGGGCCCTCCATGGCACCCTGGGCCTGTCCCCCA  2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2984  TGGCCCCACCCTGCCTGTCCTCCTCGCGGGCCCTCCATGGCACCCTGGGCCTGGGGTCCCCA  3043

Qy   2941  GGGTCTCAGAGCTCCCCCTGGCCTCGAGCCCCACCTCAGACTCA  3000
           |||||||||||||||||||||||||||||||||||||||||||
Db   3044  GCATCTCAGAGCTCCCCCTGGCCTCGAGCCCCACCTCCAGACTCA  3103

Qy   3001  GAGCCCCTGCCTCGGGAGGAGACCTCTGCTGAGCCCAGCACCCCCTGCCTCCCCTCCT  3060
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Db   3104  GAGCCCCTGCCTCGGGAGGAGACCTCTGCTGAGCCCAGCACCCCCTGCCTCACC-CCTCCT  3163

Qy   3061  TCTGAGGAAGGGCTAGGACTGGGGCGCCCGCAGCCGCCAGGCTACCAGC  3120
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db   3164  TCTGAGGAAGGGCTAGGACTGGGGCGCCCGCAGCCGCCAGGCTACCAGC  3223

Qy   3121  ACTGGAGAGCCCCACCAGGGTCAGGGGGCCTGGCCTGGCCTGGGACCCCACAGCCTG  3180
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Db   3224  ACTGGAGAGCCCCAGCCCGCCAGTGTCAGGGGGCCTGGCCTGCGGTGCTCTACCACCTGTCCGGGCACCCACAGCCTG  3283

Qy   3181  CTGCAGAAGCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA  3240
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Nucleotide sequence alignment (Qy / Db) with match bars. Representative rows:

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Qy	1741	1800
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Db	1801	1860
Qy	1861	1920
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Qy	1921	1980
Db	1921	1980
Qy	1981	2040
Db	1981	2040
Qy	2041	2100
Db	2041	2100
Qy	2101	2160
Db	2101	2160
Qy	2161	2220
Db	2161	2220
Qy	2221	2280
Db	2221	2280
Qy	2281	2340
Db	2281	2340
Qy	2341	2400
Db	2341	2400
Qy	2401	2460
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Qy	2461	2520
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Qy	2521	2580
Db	2521	2580
Qy	2581	2640
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Qy	2641	2700
Db	2641	2700
Qy	2701	2760
Db	2701	2760

Qy/Db	Start	End
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Db	601	660
Qy	561	720
Db	561	720
Qy	721	780
Db	721	780
Qy	781	840
Db	781	840
Qy	841	900
Db	841	900
Qy	901	960
Db	901	960
Qy	961	1020
Db	961	1020
Qy	1021	1080
Db	1021	1080
Qy	1081	1140
Db	1081	1140
Qy	1141	1200
Db	1141	1200
Qy	1201	1260
Db	1201	1260
Qy	1261	1320
Db	1261	1320
Qy	1321	1380
Db	1321	1380
Qy	1381	1440
Db	1381	1440
Qy	1441	1500
Db	1441	1500
Qy	1501	1560
Db	1501	1560
Qy	1561	1620
Db	1561	1620
Qy	1621	1680
Db	1621	1680

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Qy   2761  GCATCGGGAGAGGGGCCGTGCCCAGCACCTTCCGGGCTTCTGCAGCCTGTGCGTG  2820
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Db   2761  GCCTCAGGAGAGGGGCATGCCCAGCACCTTCCGGGCTTCTGCAGCCTGTGCGTGTG  2820

Qy   2821  GACACTGGGCATCCTCCTACTGCCTGGGGCCTCCTCCCCAGTCTGGCTGTCTTGAGTGGGACT  2880
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Db   2821  GACACTGGGCATCCTCCTACTGCCTGCGAGCCTCGTGCTCTGCTCGTCTTGAGTGGGACT  2880

Qy   2881  TGGCCCCACCCTCGTCCTCCTCCCCTCATGGCACCCTGGCCCTGGGGTCCCCCA  2940
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Db   2881  TGGCCCCACCCTCGTCCGGGGCCTCCTCATGGCACCCTGGCCCTGGGGTCCCCCA  2940

Qy   2941  GCGTCTCAGAGTCCCCCTGGCCTGAGCCAGCTTTCTGGAGCCTCCACCTCAGACTCA  3000
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Db   2941  GCATCTCAGAGTCCCCCTGGCCTGAGCCAGCTTTCTGGAGCCTCCACCTCAGACTCA  3000

Qy   3001  GAGCCCCCTGCCTCAGGAGACCTCTGCTCTGCTCTGAGCCCGGCACCCTGCCTCCT  3060
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Db   3001  GAGCCCCGCTGCCTCAGGAGACCTCTGCTCTGCTCTGAGCCCGGCACCCTCCTCCT  3060

Qy   3061  TCTGAGGAAGGGGCTAGGACTGGGCCCCAGAGCCGTGAGCCGGCTACCAGC  3120
           |||||||||||||||||||||||| ||||||||  | |||||||||||||
Db   3061  TCTGAGGAAGGGGCTAGGACTGGGCCCCACCCCGCCCGGACCCCCCACAGCCTG  3180

Qy   3061  ACTGGAGAGCCCCCCACCACCACCGGGCGTAGGACTGGGCCCATTGGCTCTGGCCATGGCTCTGGCACAGTCCAGGCTGCCAGTGCCAGTGCCAGGAAGAGGC  3240
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061  ACTGGAGAGCCCCCGGCCCCGCCCCAGTGTCAGGGGCCTGGGGCCCTGGGGCCTCTCGGCCACAGTCCAGGCTGCCAGTGCCAGTGCCAGGAAGAGGC  3240

Qy   3241  ACAGGGGTC  3249
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Db   3241  ACAGGGGTC  3249
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RESULT 6
US-09-600-776-9
; Sequence 9, Application US/09600776
; Patent No. 6326168
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/600,776
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: JP P1998-011434
; PRIOR APPLICATION FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR APPLICATION FILING DATE: 1998-12-04
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 3715
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-600-776-9

Query Match   81.9%; Score 2664.8; DB 4; Length 3715;
Best Local Similarity   89.0%; Pred. No. 0;
Matches 2905; Conservative   0; Mismatches 347; Indels 12; Gaps 2;

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Qy      1  ATGCCGGCCATGCGGGGGCCTTCGGGGCCTTCCTGGACAACACCTTCCTGGACACCCTACG  60
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Db    156  ATGCCGGCCATGCGGGGGCCTTCCTGGCCCCAGAACACCTTCCTGGACACCCGCACC  215

Qy     61  CGCTTTCGACGGCACGCACGCAGTAACTTCGTGGGCCAACGGCCCAGTAGTGGCCCAGGTCTTC  120
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Db    216  CGCTTCGACGGGACGCACGCAGTAACTTCGTGGGCCAACGCCCCAGTAGTGGCAGGGGTCTTC  275

Qy    121  CCCGTGGTCTACTGCTCTGTGACCTGCGATGGCTTCTGTGTGACCTGTGCTCTCCGGGGCTTCTGCAGGTC  180
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Db  1356  GAGCTGGCACGCAGGCTGGAGACGGCCCTATTACCTGGTGAGCCTGGAGTCCAGATGCGAGGG  1415

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Db  1416  AACAGCTCTGCCAGAGTGCAAAACTGCAGTAGCAGTGGCGGCGGCAGCCAGCCCAACCGGG  1475

Qy  1312  ACGGGGCTGGAGC-GCTGCGGGCGGCCGTCGCGCAGCGCGCCTACACCTCCCTCTAC---T  1371
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Db  1476  ACTGGGCTGGAGCTGCTGCCCATCCTACGCAGCGCGCTACACCTCCCTTGTAC  1535

Qy  1372  TTCGGACTCAGCAGCCTCCACCAGCGTGGGCTTCGGGAACGTGTCCGCCAACACGGACACC  1431
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Db  1536  TTCGGGCCTCAGCAGTCTCCACCAGTGTGGGCTTCGGGCTTCGGCCATGTGTCCGCCAACAGACACT  1595

Qy  1432  GAGAAGAGATCTTCTCCAATGCTCCGACCATGCTCCGCGCCCTGCGGCGGGTGGTGTT  1491
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Db  1596  GAGAAGAGATTTTCTCCAATCCTGCCGACCATGCTCTATTGGAGCTCTTATTGCAGTGGTGTTT  1655

Qy  1492  GGGAACGTGACGGGCCATCATCCAGCGCACGTACGCCCGCGGCTTTCTGTACCACAGCGGC  1551
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Db  1656  GGGAATGTGACAGCGCCATCATCCACCGCTCGTACGCCCGCGTTTTCTGTACCACAGCGGC  1715

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Db  1716  ACCCGGTGACCTGCCGAGACTACATTGCGCCATCCCACCGTATCCCCAAGCCCCTCAGCAGCGC  1775

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Db  1776  ATGCTCGAGTACTTCCAAGCCACCTTGCGCAGCCGTGAACAACCGATACCACTGAGCTG  1835

Qy  1672  CTGCAGAGCCTGCCTGACGAGCTGCGCGCAGAGCATGCGCATCCTGCCCATGCACAGGAGTC  1731
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Db  1836  CTGCAGAGCCTGCCTGACGAGCTGCGCAGAGCATGCGCATCCTGCCCATGCACAGGAGTC  1895

Qy  1732  CTGCAGCTGCCACTGTTTGAGGCGGCAGCCAGCACTGTCGCTGCGGCCACTGTCTCTGGCC  1791
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Db  1896  CTGCGTGGCCATTGTTCGGAGCGGCAGCCAGCCGCCGTGCCGGCCGTGTCTCTGGCC  1955

Qy  1792  CTGCGGGCCGCCTTCTGCACGGCCGGAGGGCTGAGTACCTCCAGCCCTGAGATGCCGGTCCAG  1851
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Db  1956  CTGAGCCCCGCCTTCTGCACGGCCGGAGTACTCATTCACCAAGCCGATGCTGCTCCAG  2015

Qy  1852  GCCCTCTACTTTGCTGCTCTGGCTCCATGGGAGGTGCTCAAGGTGGCACCGTGCTCGCC  1911
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Db  2016  GCTCTCTACTTTGTGTGTCCAGGTTCCATGGAGGTGCTCAAAGTGGGGGACCGTCCTCCC  2075

Qy  1912  ATCCTAGGGAAGGGCGACCTGATCGGCTGTGAGCTGCCGCCCGGGCAGGTGGTAAAG  1971
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Db  2076  ATTCTAGGGAAGGGCTCACAACCTGATCGGCTGTGAGCTGCCGCCCGGGCAAGTAGTGAAG  2135

Qy  1972  GCCAATGCCGACGTGAAAGCCCTGCTGTCGCTGACGTACGCGCGTCCTGCAGCCTGGCTGGC  2031
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Db  2136  GCCAATGCCGACGTAAAGCCCCTGCTGTCCCTGACGTACTCCCCTACAGTTGCCCTGGCTGGCTGGCG  2195

Qy  2032  CTGCACGACAGCCTTGCGCTGTACACCGCTGAGTTTGCCCGCGGCTTCAGTCGTGCCGAGA  2091
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Db  2196  CTGAGTCACGAGACCCTGCAGTCCCCCGTGAGTTTGCCCGCGTTTAGCCGGAGGGGCTCCA  2255

Qy  2092  GGGGAGCTCAGCTACAACCTGGTCGTGTCGGGAGGCGGCTCTGCAGAGGTGGACACCAGCCC  2151
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Db  2256  GGGGAGCTCAGCTACAACACCTGGTCGTGTCCGGGAGGTGTCCAGAGGTGATACCAGCTCA  2315

Qy  2152  CTGAGCGGGCGACAATACCCTTATGTCCAGCCCCGTCTCCCAGCTGAGGGAGAAGCAGAGGACCAG  2221
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Db  2316  CTGAGTGGTGACAACAACACCCCATGTCCACACTGGAGAAGGAGGAGCAGCAGATGGGGAGCAA  2375

Qy  2272  TGCAACCTCCTCATCCTCAGCTGCCAAGCTGCTATCCCCACGTCGAACAGCACCCCGGCCT  2231
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Db  2436  TGTACCTCCTCCTCCTCAGCGGCGGCCAAACTACTTCCCCCACGTCGAACTGGAACTGTCACCCCGCCG  2495
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Qy  2332  CGTCTAGGTGGCGAGAGGAGGGAGGCCAGGAGGGCAGGGCACGGGGCTTGAAGGCTGAGGCTGGCCCC  2391
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Db  2496  AGGCTGGGTGGCAGAGGCGGCGGCCAAGTAGGCGGGGTTTGAAGCTGAGGGGTTTGAAGCTGAGGCTGGTCCT  2555

Qy  2392  TCTGCTCCCCCACGGCGGCCTAGAGGGCTACGGCTGCCCCATGGCATGGAATGTGCCC  2451
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Db  2556  TCTGCTCATCCACCACGCACCCCTCACTTGATGGGTTGCAGCTGCCCCATGCCATGGAATGTTACCT  2615

Qy  2452  CCAGATCTGAGCCCAGGTAGTAGATGCCATTGAAGAGCGGCTGTGGCTGCGGACCAGCCC  2511
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Db  2616  CCAGACCGAGCCCAGGTCGTAGATGCCATTGAGGAGCTGCGGACCAGCCAC  2675

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Db  2676  AAGTTCTCTTCCGGGTGGTCAGTCTGGTGCCAGAATGTGAGCGCCCCAGGA  2735

Qy  2572  CCAGAGAGCGGCCTGCTCACTGTTCCCACTGGCCAAGGAACGACAGAACACA  2631
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Db  2736  ACAGAGAGTGGCGTCGTGCACTGTCCCCAGGCGTGAGGCAAGAAACACAGACACA  2795

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Db  2796  CTGGACAAGCTACGGCAGGCGGTGACGGAGCTGTCTGAACAGGTGCTCGAGATGCGAGAG  2855

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Db  2856  GGACTGCAGTCACTTCGGCAGGCTGTGCATCCTGGTGCCCAGCCACCTCCGGCCTCTGCAGCCT  2915

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Db  2916  TGTCCCGGGTATCAGGAGAGGGGCCATGCCAGCCACTGCCTTCTCTGGGCTCTCTACAACCC  2975

Qy  2812  CTGTGTGTGGACACTGGGCATCCTCCTACTGCCTGCCAGCCCCACTGCTCCTGCTCTGCTTG  2871
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Qy  2872  AGTGGGACTTGCCCCACCCTGCTCCCGGGCCT---CCTCCCCTCCCCGGCCACCCTGGCCCC  2928
          |||||||||||||| | | || ||||| ||| |  | ||||| | || |||| |||||||||
Db  3036  AGTGGGACTTGCCCTGGCCATCCACCCCGTCCACCGGCCATCCCCCTCCCCGGCCACCCTGGCCCC  3095

Qy  2929  TGGGGTCCCCAGCAGTCTCCCATGAGCCTCCCTCAGAGCGTCTCCAGGGTCTCGGCC  2988
          |||| |||||||| | |||  |  | || | || ||||| |  |||||||||  |||
Db  3096  TGGGGCCCCCAGCAGCATCCAGAGCCTCAGAGCCTCGGAGCCCTCGGAGGGTCCACCTCC  3155

Qy  2989  ACCTCAGACTCAGCCCCTGCTCCTCCAGGGACCTCTGCTCGGACACCCTGCC  3048
          ||||||||||||||||   ||| || |||||| ||| ||||||||||| |||
Db  3156  ACCTCAGACTCAGCCCCTGCTCCTCCTCGGAGACCTCTCGTCGGACACCCCAGCC  3215

Qy  3049  TCCCCTCCTCCTTCTGAGGAAGGGCTGTCGCTGCTGGCCGCAGAGCCTGTGAGCCAGGCT  3108
          |||||| ||| |||||||||||||  |   || |||||||||| || || ||||||||||
Db  3216  TCACCCCCTCCTCCTTCTGAGGAAGGAGAGTCTCCTACAGTGGACTAGGACTGGCCAGGCT  3275

Qy  3109  GAGGGCTACCAGCACTGGAGAGCCCCACCCAGGGTCAGGGGGAC  3168
          |||||||||| ||| |||||||||||| |||  | ||||||||
Db  3276  GAGGGCTACCAGTACTGAGAGCTGAGAGCCCCCCCCAGGGGGCCAGCCTTGCCGGGCCCAGTCCTGGGAT  3335

Qy  3169  CCCCACAGCCTGGAGATGGTGCTTATTGCTTGCTGCTGCACAGTCCAGTGGACC  3228
          |||||  ||| || ||  | |  | ||||||||  | ||||||||||||||||
Db  3336  CCCCAGCAGCCTAGAGATGGTGTCTCATCGGCTGGGATACCAGTCCAGTCGGTCCGGTCCAGGACC  3395

Qy  3229  CAGGAAGAAGGCACAGGGGTCTGA  3252
          |||||| ||||||| ||||||||
Db  3396  CAGGAGGAGGGGCACAGGAGTCTGA  3419
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; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/600,776
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: JP P1998-011434
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 5
; LENGTH: 3064
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(3057)
US-09-600-776-5

Query Match         27.2%;  Score 884.8;  DB 4;  Length 3064;
Best Local Similarity  65.5%;  Pred No. 7.2e-177;
Matches 1408;  Conservative  0;  Mismatches 622;  Indels 120;  Gaps  3;
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Qy   1855  CTCTACTTTGTCTGCTCCATGGAGGTGCTCAAGGGTGCACCGTGCTGCCATC 1914
                 | |||  |||||||  |||||  |||||;||||||   |||||||||||||
Db   1780  CATTACTATGTCTGCTCCCGGCTCGCTTGAGGTGCTCCGAGACAACATGTGCTGCGCCAATC 1839

Qy   1915  CTAGGGAAGGCGACCTGATCGGCTGTGAGCTGAGCCGGAG------ 1962
                 ||  ||||||||  |||||  ||||||||||||||  ;|||
Db   1840  CTGGGGAAGGGGACCTGATTGGAGCAGATATCCCTGAGCCGGGGCAGGAGGCCTGGGTG 1899

Qy   1963  ------------GTGG:AAAGGCAATGCCAATCCAGTGCTGA:GTGAAAAGTCTGACC:ACTGT 2004
                        || | ||| ||| || ||||||;|| ||||||||| ||||||
Db   1900  GGAGCAGAGACCCAAACTTCGT:GCTAAAGACCAGTTCG:GTGAAAGCTCTGACC:ACTGT 1959

Qy   2005  GTCCTGCAGTGTCTGCAGCTGGCTGGCCACGACAGCCTTGCGCTGACAACCTGG 2064
                 || |  ||||||||||  ||||||||||||  ||| ||  ||;:|||
Db   1960  GGCCCTGCGCAGCGTGCAGCCGAGGGTCCTGAGGTCCTGAGGC:CTATCCGAG:AT 2019

Qy   2065  GCCCCGCGCTTCAGTGCGTGGCGTCCGGAGGTGCCCGAGGGGAGCTCAGCTACGTACAACCTGG 2114
                 |||  |||| ||  ||||||| |||||||||  ||| |; ;|||||;||  |
Db   2020  GGGCTGCCTCCGGGTGCGCCCCGGGACCTGCCCCGGGACCTCACCTTCAACCTGCG 2069
```

RESULT 8

US-09-600-776-10

; Sequence 10, Application US/09600776
; Patent No. 6326168
; GENERAL INFORMATION:
;   APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
;   TITLE OF INVENTION: A novel potassium channel protein
;   FILE REFERENCE: Y9903-PCT
;   CURRENT APPLICATION NUMBER: US/09/600,776
;   CURRENT FILING DATE: 2000-07-21
;   PRIOR APPLICATION NUMBER: JP P1998-011434
;   PRIOR FILING DATE: 1998-01-23
;   PRIOR APPLICATION NUMBER: JP P1998-346198
;   PRIOR FILING DATE: 1998-12-04
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 3736
;   TYPE: DNA
;   ORGANISM: Rattus sp.
US-09-600-776-10

Query Match   26.7%; Score 869.8; DB 4; Length 3736;
Best Local Similarity 65.3%; Pred. No. 1.1e-173;
Matches 1403; Conservative   0; Mismatches 527; Indels 117; Gaps   4;

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Qy     1  ATGGCCGGCCATGCGGGGCGGCCTCCTGCGCCTCCAGAACACTTCCTTGGACACCA:CGCTACG  66
             |||||||     ||||| |||  ;||| |||;|| |  ||||||||||||||;|||
Db   136  ATGCCGGTCATGAAGGCGGTTGCTGGCCACATTCTGGACACCACGCACT  195

Qy    61  CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGCAACGCCCAGGTGGGCGGGC:CTC:TTC  120
             ||||| |||||||| |||||||| ||| |||||| |||| |||||||;||||||
Db   196  CGCTTTGACGGACGCACAGCACAACTT:TCTTGTGGCCAATGCCCACGGGG:TTT  255

Qy   121  CCGTGCTGTCTACTGCTTCTGATGCCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC  180
             | ||  ||||| |;|| |||  |||| |||  | ||||  |||||  |  |||
Db   256  CCCATCGTCTACTGCTTCTGACGCGCTTCTGTGACCTTCGGGACC:CACAGGGTACGGCCGTC  315

Qy   181  ATGCAGCGGCGGGCTGTGCCTCCTTTATGGGCACAGACACCAGTGAGCCTCGTCCGC  240
             |||||  |||| ||  ||| |||||||||||||;|||||||;||
Db   316  ATGCAGAAAAACCCGTAGCTGCGCGTTCCTCCTATGGCCTCTGTGGCCTGG  375

Qy   241  CAACAGATCCGGCAGGCCTGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCCGTAC  300
             |||||  ||||||||| |||||  ||  || || ||| | ;  | |;||||
Db   376  CAACGGTTACAAAAAGCCC:GAGGGCCACCAACAAACACAGAGC:TGAAATCTG:TTTTAC  435

Qy   301  CGGAACAGCGGGCTCCCGTTCTGGTGTCTCTGGATGTGATACCCATAAAGAATGAGAAA  360
             ||| |  ||||||  | |||  ||;||  |||||||||; |||| | |||
Db   436  CGAAAGGATGCTCGGCGCGTTTTGGTGTTCTTCGTCACAGACGTCATCGATGCCCATCAAAAATGAGCTG  495

Qy   361  GGGGAGGTGGCTCTCTTCACAGGACACATCAGCGAAACCAAGAACCGAGG-  410
             |||||||  ||  ||  || |||  ||  ||
Db     1  ...
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Qy   1 ATGCCGGCCATGCGGGGCGGCCTCCTGCGCGCCCAGAACACCTTCCTGGACACCATCGCGCTACG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGCCGGCCATGCGGGGGGGCCTCCTGCGCGCCCAGAACACCTTCCTGGACACCATCGCGCTACG 60

Qy   61 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGCCCAGGTGGGCGGGCTCTTC 120
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db   61 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGCCCAGGTGGGCGGGCTCTTC 120

Qy   121 CCCGTGGTCTACTGCTTCTGTGATGGCTTCTGTGACCTCACGGGCTTCCCGGGCTGAGGTC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCCGTGGTCTACTGCTTCTGTGATGGCTTCTGTGACCTCACGGGCTTCCCGGGCTGAGGTC 180

Qy   181 ATGCAGCGGGGCTGTGCCTGCTCCTTATGGCCAGACACCAGTGAGCTCGTCGC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ATGCAGCGGGGCTGTGCCTGCTCCTTATGGCCAGACACCAGTGAGCTCGTCGC 240

Qy   241 CAACAGATCCGCAAGGCCCTGACGAGCAGCAAGAGGCTCAAGGCTGAGATCCTGTAC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CAACAGATCCGCAAGGCCCTGACGAGCAGCAAGGAGGCTCAAGGCTGAGATCCTGTAC 300

Qy   301 CGGAAGAGCGGGGCTCCGTTCTGGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CGGAAGAGCGGGGCTCCGTTCTGGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA 360

Qy   361 GGGGAGGTGGCTCTTCTTCCAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GGGGAGGTGGCTCTTCTTCCAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG 420

Qy   421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGCGGCCGATATGGCCACGATCC 480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GGCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGCGGCCGATATGGCCACGATCC 480

Qy   481 AAAGGCTTCAATGCAACCCGGAGTACAAAGTAGCCCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT 540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AAAGGCTTCAATGCAACCCGGAGTACAAAGTAGCCCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT 540

Qy   541 CTGCAGAAGCAGCCCAAGGCAACCACAAGCTCAATAAGGGGTGTTGGGAGAAACCA 600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CTGCAGAAGCAGCCCAAGGCAACCACAAGCTCAATAAGGGGTGTTGGGAGAAACCA 600

Qy   601 AACTTGCCTGAGTACAAAGTAGCCCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 AACTTGCCTGAGTACAAAGTAGCCCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT 660

Qy   661 GGGGCACTGAGAGCCACCTGGATGCTTCATCCTCGCTCGCCCACACTCTATGTGGCTGTC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GGGGCACTGAGAGCCACCTGGATGCTTCATCCTCGCTCGCCCACACTCTATGTGGCTGTC 720

Qy   721 ACTGTGCCCTACAGCGTGTGTGTGACCACAGCGAGCACGGAGAGCCCAGTGCGCCCGCGGCCCG 780
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCGAGCACGGAGAGCCCAGTGCGCCCGCGGCCCG 780

Qy   781 CCCAGCGTCTGTGACCTGCCGTGAGGTCCTCTCATCCTTGACATTGTCTGAATTC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CCCAGCGTCTGTGACCTGCCGTGAGGTCCTCTCATCCTTGACATTGTCTGAATTC 840

Qy   841 CGTACC 846
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Db   841 CGTACC 846

RESULT 10
US-09-358-383C-7
; Sequence 7, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21

Qy   1492 GGGAACGTGACGGCCATCATCCAGGCATGTACGCCCGCGTTCTGTACCACAGCGC 1551
            |||| || || ||||||||||||||| |||| ||||| || |||||||||||||
Db   1552 GGGAATGTCACAGCCATCATCCAGGCATGTACGCCCGAGCGTCTACCACAGCCGC 1611

Qy   1552 ACGCGCGACCTGCGCGACTACATCCGCGACTACCGAGATCCCCAAGCCCTCAAGCCAGCGC 1611
            ||||| ||| ||||| | |||| ||||||||| | | ||| |||||||||| ||||| |||
Db   1612 ATGAAGGGATCTCAAGGCATCATCCGAGTGCATCCGAGTCGTCTGCGCCGCGCAAGCAGCGC 1671

Qy   1612 ATGCTGGAGTACTTCCAGCCACCTGGGCGTGAACAATGCATCACCACCGGAGTC 1671
            |||||||| ||||| | || ||||||||| ||| ||| ||||||| ||||||
Db   1672 ATGCTCGAGTACTTCCAGACTACATGGGCCGTCAACGGGCCATCGATGCCAACGAGTTA 1731

Qy   1672 CTCCAGAGCCTCCCTGACGAGCTCGCGCGCAGAGATCGCCATCGACTCGCACACCAGGCCAGGGC 1731
            || | ||||| | || || || |||| | |||| ||||| |||||||| || |||||||
Db   1732 CTGCGTGACTTCCCGGATGAGCTGCGAGCTGCGAGCCGCATCAGCACCTGAATCGGGAGATC 1791

Qy   1732 CTGCAGTCGCCACTGTTTGAGGGCGGCCAGCCGCGCGCCACTGTCTCTGGCC 1791
            ||||||||||||| |||||||||| |||| ||| ||| |||||| | | |||
Db   1792 CTGCAGTCGCTGCCTTTGTTTGGAGCAGCAAGCAGCGGGGCTGCCTTCGTTCGCCTCGCTCCTGGCAC 1851

Qy   1792 CTGCGGCCGCCTTCTGCACGCCGGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAG 1851
            | | ||| ||| ||||| | || |||| |||| |||||| |||| ||| ||| |||
Db   1792 CGGCAGCCGCCTTTGTCTTTGGTGAGCAAGACAGCATGTGATGAGTAAAGAATGAGAAA 1911

Qy   1852 GCCCTCTACTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGGTGGCCACCGTGCTCCCC 1911
            ||| | ||||| || |||| | || ||||| || || | ||||||| ||| |||
Db   1912 GCACTACTATGTCGCTCTGCTCTCGGAGTCTCCAGAGGTGGTCCACGGGTGCGGG 1971

Qy   1912 ATCCTAGGGAAGGGCGACCTGAATCGGCTGTGAGCTCGCCGCGGGGGAGCAG------ 1962
            | ||| ||||||||||| || || | | || ||| || || ||| |||
Db   1912 GCCCCGACAGATGGAAGGAGACAGGTGGTGGCCGCGGCCGATATGGCCACGATCC 2031

Qy   1972 ATCCTTGGAAAGGGGACTTGATTGGGCAGACATCCTGAGTGGGGCAGGAGCCTGGG 2023
            | |||| || || ||| || | ||| | |||| | || |||||||
Db   1972 AGCCTGAGTACAAAGTAGCCCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT 2031

Qy   1963 ------GTGTAAAGCCAATGCCGACGTGAAGGGGTGACGTACTGCGTC 2007
                  ||||| || || | ||| | | | || || ||||||
Db   2032 GCAGGGGCAGGCTCGCGTGCTGAAGACAGCAGCCCTGA-GTGAAAGCACTGACTTACTGGG 2091

Qy   2008 CTGCAGTCTGCGCAGCTCGGCTGCTCGCACCACACAGCGTTGGCGTGTACCCCGAGTTTGCC 2067
            ||||| || || ||| || ||| ||| || || || ||| ||| | |||||||||
Db   2092 CTGCAGCAGCTGAGCAGCCGAGGCTGCCGAGGCTCCGCAGGGCTGCCTTGTATCCGGAATATGTG 2151

Qy   2068 CCCGGCTTCAGTCGTGCGTGCCCTCCGAGGGGAGCTCAGCTACAACCTGGG 2114
            ||||| ||||| |||| | ||||||| ||||||||||||||||||||||
Db   2152 GCTGCCTTCAGGGCTGCGGGGCTGGCCTTAACCTTCAACCTGCGG 2198

RESULT 9
US-09-358-383C-9
; Sequence 9, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (:)..(870)
US-09-358-383C-9

Query Match   26.0%; Score 844.4; DB 4; Length 870;
Best Local Similarity 99.9%; Pred. No. 1.6e-168;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
NUMBER OF SEQ ID NOS: 36

; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 7
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (263)..(1132)
US-09-358-383C-7

Query Match   26.0%;   Score 844.4;   DB 4;   Length 1132;
Best Local Similarity 99.9%;   Pred. No. 1.7e-168;
Matches 845;   Conservative 0;   Mismatches 0;   Indels 1;   Gaps 0;

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Qy      1 ATGCCGGCCATGCGGGGCCTCCTGGCCGCCTCAGAACCACTTCCTGGACAACACCTTCCTACG  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    263 ATGCCGGCCATGCGGGGCCTCCTGGCCGCCTCAGAACCACTTCCTGGACAACACCTTCCTACG  322

Qy     61 CGCTTCGACGGCACGCACGCCACAGTAACTTCGTGCTGGGCAACGCCCAGGTGGCGGGGCTCTTC  120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    323 CGCTTCGACGGCACGCACGCCACAGTAACTTCGTGCTGGGCAACGCCCAGGTGGCGGGGCTCTTC  382

Qy    121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGGCTTCTCCCGGGCTGAGGTC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    383 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGGCTTCTCCCGGGCTGAGGTC  442

Qy    181 ATGCAGCGGGGCTGCCTGCCTGCTCCTTTATGGGCCAGACACCAGTGAGCTCGTCCGC  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    443 ATGCAGCGGGGCTGCCTGCCTGCTCCTTTATGGGCCAGACACCAGTGAGCTCGTCCGC  502

Qy    241 CAACAGATCCGCAAGGCCCTGGACAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC  305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    503 CAACAGATCCGCAAGGCCCTGGACAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC  562

Qy    301 CGGAAGAGCGGGGTGCCTCCGTTCCGGATGTGATACCATAAAGATGAGAAA  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    563 CGGAAGAGCGGGGTGCCTCCGTTCCGGATGTGATACCATAAAGATGAGAAA  622

Qy    361 GGGGAGGTGGCTCTTCTCCTAGTCTCCACAAGGACATCAGCGAAACCAAGAACCGAGGG  420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    623 GGGGAGGTGGCTCTTCTCCTAGTCTCCACAAGGACATCAGCGAAACCAAGAACCGAGGG  682

Qy    421 GGCCCGACAGATGGAAGGACACAGTGGTGCCGCCGGGCCCGACGATCC  480
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    683 GGCCCGACAGATGGAAGGACACAGTGGTGCCGCCGGGCCCGACGATCC  742

Qy    481 AAAGGCTTCAATGCCAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTCCACTGT  540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    743 AAAGGCTTCAATGCCAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTCCACTGT  802

Qy    541 CTGCAGAAGCAGCCCAAGGCACAAGCAGCGCCATCCGGAAGTCGCCCTCATGTGGCTGTC  600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    803 CTGCAGAAGCAGCCCAAGGCACAAGCAGCGCCATCCGGAAGTCGCCCTCATGTGGCTGTC  862

Qy    601 AACTTGCCTGAGTACAAAGTAGCCCGACTTCCGGAAGTGCGCCCCACCGGCCCCCCGGGCCCCG  660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    863 AACTTGCCTGAGTACAAAGTAGCCCGACTTCCGGAAGTGCGCCCCACCGGCCCCCCGGGCCCCG  922

Qy    721 ACTGTGCCCTACAGCGTGTGTGTGAGCACAGCCAGCACGGGAGCACCGTCGCGGCCCG  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    923 GGGCCACTGAGAGCGCCTGGGATGCCTCATCCTGCTCGCCACACTCTATGTGGCTGTC  982

Qy    781 CCCAGCTGCTGTGACCTGGAGGTCCTTCATCCTTGACATGTGCTGAATTTC  840
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    983 ACTGTGCCCTACAGCGTGTGTGAGCACAGCCAGCACGGGAGCACCGTCGCGGCCG  1042

Qy    841 CGTACC  846
          ||||||
Db   1043 CCCAGCTGCTGTGACCTGGAGGTCCTTCATCCTTGACATGTGCTGAATTTC  1102

                 CGTACC  846
                 ||||||
Db           CGTACC  1108
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Db   1103 CGTACC 1108

RESULT 11
US-09-358-383C-17
; Sequence 17, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 17
; LENGTH: 3321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3321)
US-09-358-383C-17

Query Match   23.4%;   Score 761.2;   DB 4;   Length 3321;
Best Local Similarity 62.2%;   Pred. No. 6.7e-151;
Matches 1319;   Conservative 0;   Mismatches 708;   Indels 93;   Gaps 4;

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Qy      1 ATGCCGGCCATGCGGGGCCTCCTGGCCGCCTCAGAACACCTTCCTGGACAACACCTTCCTAGCGTACG  60
          |||||| |||  |   ||    ||| |||||||||   ||||| ||||| |||||||||||
Db      1 ATGCCGGTTATGAAAGGATTACTGGCGCCGCCCAAAACACCTTCCTGGACAACACCCGCCACC  60

Qy     61 CGCTTCGACGGCACGCACGCCACAGTAACTTCGTGCTGGGCAACGCCCAGGTGGCGGGGCTCTTC  120
          ||| ||||| |||  |   |  |   ||  ||| |||    ||  ||||||||||| |||| ||
Db      1 CGTTTGACGGAACAACATAGCAACTTCATCCTTGCTGCGAGCTTGCTGGATTGCCCGAACTGAAGTC  120

Qy    121 CCCGTGGTCTACTGTCTCTGATGGCTTCTGTGACCTCAGCGGGGCTTCTCCCGGGCTGAGGTC  180
          |||  || ||| || ||  |   ||| ||| ||  |  ||  ||||    ||| |  ||| |
Db    121 CCCATAGTCTACTGTTCCGATGGCTTGCTGCGAGCTTGGATTGCCCGAACTGAAGTC  180

Qy    181 ATGCAGCGGGGCCGTGCCGCTGCTCCTTTATGGGCCACAGGAGTTCAAGGAATGAATGAGAAA  240
          ||| || || | ||||| |  |  |  ||| |||| || ||  ||  |||  | |  || |||
Db    181 ATGCAGAAGAGTTGTAGCTGGCAAGTTCTTATTTGGGTGAAACCATGAGCAACTGATG  240

Qy    241 CAACAGATCCGCAAGGCCCTGGACGAGCAGCACACAAGGAGTTCAAGGACGTGATCCTGTAC  300
          |  |  | |  |  ||||| | | ||   |   | || ||    |||  |  | | ||| ||
Db    241 CTTCAAATAGAAAGTCACTGGAGGAGAAACAGAATTCAAAGGAGAAATTATGTTCTAC  300

Qy    301 CGGAAGAGCGGGGTCTCCTGGATGTGATAACCATAAAGAATGGAGAAA  360
          || | |  ||||   |  ||  |  |  |||  | | ||  | ||| ||
Db    301 AAGAAAAACGGGTCTCCATTTTTGGTGCCTACTGGATATTGTTCCCATAAAGAATGAATGAAAAA  360

Qy    361 GGGGAGGTGGCTCTTCATCCTGTTCCACTGT  420
          |||  | | ||||  |   | | | || ||
Db    361 GGAGATGTAGTACTTTTTCTGCCTCGTTCAAAGATAACAGATA-CAAAAGTGAAGAT  419

Qy    421 GGCCCCGACGATGGGAGGAGACAGCAGTGGTGGCGCACGATCC  480
          ||||| |  | ||| | || |||| | | ||| | | |  |||
Db    420 GGCCCCGACGATGGTGGGAAAGGAGATCAAGACAGGGACCCA---  476

Qy    481 AAAGGCTTCAATGCCAACCGGGCCGAGCCCGGGCCCGGGCCCCGCCGGGCAC  540
          ||| |  |  |     ||| |  |  ||| | ||  |  | || | | | |||
Db    477 -----CTTTGCTGTCACGCCGGAGTCGAGCAGTGCAGTCCTTTATCACATCCTCTGGGCAC  531

Qy    541 CTGCAGAAGCAGCCCAAGGGTGTTTGGGGAGAAACCA  600
          || || || || |  ||||| | |||| | || |||
Db     54 CTGCAGAAGCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGGTGTTGGGGAGAAACCA  600

Qy    601 AACTTGCCTGAGTACAAAGTAGCCGACTTCCGGAAGTGCGCCGGTGTTGGGGAGAAACCA  660
          ||||||||||||||||||  ||||| |||  || | | ||| |||| ||| |||  ||||
Db    532 CTGCAAAGAGAAGAAGAAACAAATGAAAATAAATAACAATGTTTTTGTAGATAAACCA  591

Qy    601 AACTTGCCTGAGTACAAAGTAGCCCGCCACTCCGGAAGTGCGCCCTCATCCTGTTCCACTGT  660
          ||||| |||||||||||||||| ||| ||||||||||||||||||||||||| |||||||||
Db    592 GCATTTCCGGAGTATAAAGTTTCTGATGCAAAAAAAGTCCAAATTCATCACTTCTCGCATTTT  651
```

```
Qy   1741 CCACTGTTTGAGGGGCCAGCCGGCGGCTGCGTCGGGGCACTGTCCTGGCCCTGCGGGCCC 1800
          ||||||| |||||||       |||||||   |||||||||||||||   | ||||||||
Db   1648 TCCCTTTTGAATGTGCCAGCCGGGCTGCCACCAAGGCTCTGTCTCTCTCTACACATCAAAACC 1707

Qy   1861 GCCTTCTGCACGCCGGCCGGCGAGTACCTCATCCTCCAAGGCGATGCCCTGCAGGCGCTCTAC 1860
          | ||||| ||||||| ||| |||||| | ||||||||   |||||||||  |||||||||||| 
Db   1708 TCTTGTCTGCTCCGGGGAGTATCGTCTGCGCATCGCTTCAAGGGGATGCCTCATCCTTCAGCCATCCTAC 1767

Qy   1861 TTTGTCTGCTCTGGCTCCATGGAGGTGCTCAAGGTGGCGACCGTGCTCGCCATCCTAGGG 1920
          |||||||||||   |||||||||||| ||||| |||  |||| ||||||||||| ||||| 
Db   1768 TTTGTATGCTCGGGCGCTCCATGGAGAGTTCTTAAAGACAGCCATGGTGCTCGCTATCCTTGGG 1827

Qy   1921 AAGGGCGACCTGATCGGCTGTGAGCGTCCCCGGGAGCAGGTGGTAAAGGCCAATGCC 1980
          |||||||||||||||||||  |||||||   ||   |||||||||||  |||||||| 
Db   1828 AAAGGGGATTTAATTGGAGCAAATCTATCAATTAAGGACCAAGTGATCAAGACCAATGCA 1887

Qy   1981 GACGTGAAGGGGCCGACGTACTGCGTCCTGCAGTGTCTGCAGCGTCTGGCCTGCACGAC 2040
          |||| ||||||| |||||||||||  ||||||||  |||| ||   ||||||||||||| 
Db   1888 GATGTAAAGGCTTTAACCTACTGTGATCTCCAGTGTATCATCCTCAAAGGACTCTTTGAA 1947

Qy   2041 AGCCTTGCCGTGTACCCGGTTGCCCCGCGCTTCAGTCGTCGTCGTCCGAGGGGAGCTC 2100
          ||| ||||||| ||| ||| |||  |||||   ||| ||| |||| |||| ||||||| 
Db   1948 GTGGTAGACCTTTACCCAGGATATGCTCACAAATTGTGGAAGACATTCAGCATGACCTC 2007

Qy   2101 AGTACAACCTGGTGCTGG 2120
          ||||||||||||||||||
Db   2008 ACATACAACCTCCGAGAGG 2027
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```
RESULT 12
US-09-358-383C-15
; Sequence 15, Application US/09358383C
; Patent No. 6518898
; GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-055CP
;  CURRENT APPLICATION NUMBER: US/09/358,383C
;  CURRENT FILING DATE: 1999-07-21
;  PRIOR APPLICATION NUMBER: USSN 09/119,855
;  PRIOR FILING DATE: 1998-07-21
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;  LENGTH: 5107
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (196)..(3516)
;  NAME/KEY: misc_feature
;  LOCATION: 4777
;  OTHER INFORMATION: n = a,g,t or c
US-09-358-383C-15

  Query Match             23.48%;  Score 761.2;  DB 4;  Length 5107;
  Best Local Similarity   62.28%;  Pred. No. 7.5e-151;
  Matches 1319;  Conservative  0;  Mismatches  708;  Indels  93;  Gaps  4;
```

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Qy      1 ATGCGGCCATGCGGGGCCTCCTGGGCCTCCAGAACACCTTCCTGGACACCAGCTGCTACG 60
          ||||||    ||||||||  ||||| ||||||||||||| |||||||||||||| ||||| 
Db    196 ATGCGGTTATGAAAGGATTACTGGCCCCGCAAAACACCTTCCTGGACACCAGCCTGCCACC 255

Qy     61 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGTGGCACGCCAATGCGGGGCTCTTC 120
          |||| |||| ||||| |||||| ||||||||||||||||||||||  |||||| |||
Db    256 CGTTTTGACGGACAGAACAGATAGCAACTTCATCCTTGTGCACTCCAGGTGCTAAGGGTTTC 315

Qy    121 CCGGTGGTTCTACTGCTCTGATGGCTTCTGTGACCTCCCGGGCTGAGGTC 180
          |||||||||||||||||| || |||||||||||||||| ||| || |||
Db    316 CCCATAGTCTACTGTTCCGATGGCTTCCGATGGCTTCTGCGGAGTTGCCCGAACTGAAGTC 375

Qy    181 ATGCAAGCGGGGCTGTGCCTGCTCCTTTTATGGGCCAGACACCAGTGCGTCCGC 240
          ||||| ||    ||   || ||||||  | ||    ||
Db
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Db    376  ATGCAGAGAGACTTGTAGCTGCAAGTTCTTATTTGGGGTTGAAACCAATGAGCAACTGATG  435

Qy    241  CAACAGATCCGCAAGGCCCTGGACGAGCCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC  300
                                                                          
Db    435  CTTCAAATAGAAAAGTCACTGGAGGAGAAAACAGAATTCAAAGGAGAAATTATGTTCTAC  495

Qy    301  CGGAAGAGCCGGGCCTCCGTCTCCTGGATGTGATACCCATAAAGAATGAGAAA  360
                                                                          
Db    496  AAGAAAAACGGGTTCTCCATTTTGGTGCCTACTACTGGGATATTGTTCCCATAAAGAA GAAAAA  555

Qy    361  GGGGAGGTGGCTCTCTTCCTAGTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG  420
                                                                          
Db    556  GGAGATGTAGTACTTTTTCTGGCCCGTTCAAAGATATAAACAGATACAAAAGTGAAGAT  614

Qy    421  GGCCCGACAGATGGAAGGAGCAGGTGTGCGGCGCGCCGATATGGCCGGCCACGATCC  480
                                                                          
Db    615  TACTCCAGAAGATAAAAAACAAGAAGACAAGAGATCAAGAGAGCCAGGGGACCCA  671

Qy    481  AAAGGCTTCAATGCCAACCCGGGCGGCCGTGCTCTACCACCGTCTCGGGCAC  540
                                                                          
Db    672  CTTTGACTCAGCCCGAGACGGAGTCGAGCAGTCCTTTATCACAICTCTCGGGCAA  726

Qy    541  CTGCAGAAGCAGCCCAAGGCACAAGTCAATAAGGGGTGTTGGGAGAAACCA  600
                                                                          
Db    727  CTGCAAAGAAGAGAAAGAACAAATTGAAAATAACAATGTTTTTGTAGATAAAACCA  786

Qy    601  AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTGCCCCTCATCCTGTTGCACTGT  660
                                                                          
Db    787  GCATTTCCGGAGTATAAAGTTTCTGATGCAAAAAGTCCAAATTCAICTCTCTGCAITTT  846

Qy    661  GGGGCACTGAGAGCCAAGCTTCAICTCTGCTCGCCACAICTAICTGCCTGTC  720
                                                                          
Db    847  AGCACTTTTAAAGCTGGCTGGGACTGGCTTATTTGTTGGCAACGITTTTATGTTGCTGTG  906

Qy    721  ACTCTGCCCTACACGCTGTGTGTGAGCACAGACGGAGCCCAGTGCCGCCCGGGGCCCG  780
                                                                          
Db    907  TCTTTCTGTCTCCTACAACGTTTGCTTTATTGGCAATGACGACCTGGTCCCACAACTCGGAGC  963

Qy    781  CCCAGCGTCGTGTGACCTGGCCTGGGAGGTCCTCTCATCCTTGACATTGTGCTGAATTTC  840
                                                                          
Db    964  ACAACCGTGTCAGTGACATTGAGTTGAGAGATTCTTTTATTATAGATATTTTTAAAATTIC  1023

Qy    841  CGTACCACATTCGTGTCCAAGGTGCTGTTGCCCAAAGICCATTGCCTC  900
                                                                          
Db   1024  CGAACAACTTATGTCAGCAGATCTGCCAAGTTATCTTTGAAGCAAGATCAATTTGCATC  1085

Qy    901  CACTACGTCGTGTGACCTGGTTCCTGGATGTCATCGCCCCTTGACCTGCTA  960
                                                                          
Db   1086  GATGTAAAGGCTTTAACCTACTGTGATCTCCAGTGTATCATCCTCAAAGGACTCTTTGAA  1143

Qy    961  CGTACCCACCGAGTTGCGGGCCCATCTGCTGAAGACGGTGCGCCTGCTG  1020
                                                                          
Db   1144  TATGCTTTCAAGCTGCTGCTCTCGTGTCTCCGTGCATGTTTCTAAAGACAGTGCGCCTCTTG  1203

Qy   1021  CGCCTGCTGCCGCTGTTGCGCCCACTGGGCCGTGGGTGTCGTTTTAC  1080
                                                                          
Db   1204  CGTCTTTTGCGICTGCTGCTCGAGAAGTTAGACCGGCTATTCCCAACACAGTACTCGTCCTG  1263

Qy   1081  ACACTGCTCCATGGCCGTGTTCGCCCACTGGTCTCGCGCACTGGGTTTTAC  1140

Qy   1141  ATTGGCCAGCCGGGGCAGATCCAGGCAGCAATCCAGCGCGACAGACCTTCGAGACGGCGTGTTTAC  1200
                                                                          
Db   1324  ATTGGAAAAATGGAGGGAGGGAGCACAACAGCCTTCTGAAGTGGGAAGTTGGTTGGCTTCAT  1383

Qy   1201  GAGCTGGCCGCCGACTGGAACTCCACTACCTCCTTTGGGGCCGCAGCCAGTGGGAGGG  1260
                                                                          
Db   1384  GAGTTGGGAAAGACGACTGGAATCTCCATACTAT  1416

Qy   1261  AACAGCTCCGGCCAGAGTGACAACTGCAGCACGACGAGGGCCAACCGGACGGGGCTG  1320
                                                                          
Db   1417                                                        GGCAAC  1422
```

```
Qy   1321  GAGCTGCTGGCGGCCGTGCTGCCTCGGGCAGGCGGCTACATCCCCTTAC TCGCCACTC  1380
                                                                          
Db   1423  AA ACCTTGGGGGGCCCGTCGATCCGAAGTGCCTATATTGCCCGCTCTGTACTTCACGCTG  1482

Qy   1381  AGCAGCCTCACCAGGCTGGGCTTCGGCAACGTCTCCGGCCAACACCGAGACACCGAGAAGATC  1440
                                                                          
Db   1483  AGCAGCCTCACCAGGCTGGGTTTTGGGAACGTCTCTGTTCAGATACGCAGAAAAGATC  1542

Qy   1441  TTCTCCATCGCACCATGGTCATCGGCGCCCTGATGCAGCGGTGGTGTTTGGGAACGTG  1500
                                                                          
Db   1543  TTCTCCATCGTCACCATGGTCATCGGCGCCCTGATGCAGCGGTGGTGTTTGGGAAACGTG  1602

Qy   1501  ACGGCCATCATCCAGCGCATGTACGCGCCGCGTTCGTTGTTACCACAGCCGCCACGCCGGAC  1560
                                                                          
Db   1603  ACAGCAATCATCACAGAGGATGTACTCCAGATGTCCCTCTATCACACTAGAGACTAAGGAT  1662

Qy   1561  CTGCGCGACTACATCCGGCTGTCCGGCGTTCCCAGCCCTCAAGCCCGCCATGCGGGAG  1620
                                                                          
Db   1663  CTGAAAGATTTCATCCGTGTCATCACTTGCCCCAACAACTCAAGCAGAGATGCTCGAA  1722

Qy   1621  TACTTCCAGGCACCTGGGCGGTGAACAATGGCGATCGACACCACCGTGCTCGCGAGAGC  1680
                                                                          
Db   1723  TATTTCAAACAACCTGGTCAGTCAACAATGAATAGATTCAAATGAGCTTTGAAAGAC  1782

Qy   1681  CTCCCTGACGAGCTGCGCGGAGCATCGCCATGCCATGCACCTGCACAAAGGGATGTCCTGCAGCTG  1740
                                                                          
Db   1783  TTTCAGATGAACTGCGTCTGACAATCACTATGCACTTGAACAGGAGATCTTACAGTTG  1842

Qy   1741  CCACTGTTTGAGGGCCAGCCAGGAGCATGCTGTGCCCGGGCCC  1800
                                                                          
Db   1843  TCCCTTTTTGAATGTGCCAGCCGGGGCTGCCTCAGGTCTCGTCTCTACCACATCAAAAACC  1902

Qy   1801  GCCTTCTGCACGCCGGCGGAGTGACCTACCTCCATCCCACCAAGGCGATGCCCTGCCTCTAC  1860
                                                                          
Db   1903  TCTTTCTGTCGTCCGGGGAGTATCTGCTGCGTCAAGGGGATGCTCTTGCAGGCCATCTAC  1962

Qy   1861  TTTGTCTGCTGTGGCTCCATGGAGGTGCTCAAGGTGCCACCGTGCTCTCGCCGATCCTAGGG  1920
                                                                          
Db   1963  TTTGTATGCTGCGGGCTCCATGGAAGTCTTAAAGACAGCAGGATGGTGCTGGCGTATTCTTGGG  2022

Qy   1921  AAGGGCGACCTGATCGGCTTGAGCTGCTGTCCCCGGCGGAGCCAGTCGCTGGTAAAGGCCAATGCC  1980
                                                                          
Db   2023  AAAGGGGATTTAATTGGAGCAAAATCTATCAAGTGATCAAGACCAATGCA  2082

Qy   1981  GACGTGAAGGGGCTGAGGGGGCTGACGTACTGCGTCTGCAGTGTCGTCAGCTGCGCTGCCACGAC  2040
                                                                          
Db   2083  GATGTAAAGGCTTTAACCTACTGTGATCTCCAGTGTATCATCCTCAAAGGACTCTTTGAA  2142

Qy   2041  AGCCTTGCGCGTGACCCGAGTTTGCCCCGCGCTTGCTCCGAGGGGAGCTC  2100
                                                                          
Db   2143  GTGCTAGAACTTTACCCAGAATATGCTCACAAATTGCGTGGAAGACATTCAGCGATGACCTC  2202

Qy   2101  AGTACAACCTGGGTGCTGG  2120
                                                                          
Db   2203  ACATACAACCTCCGAGAAGG  2222
```

```
; LENGTH: 1626
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(:626)
US-09-358-383C-6

Query Match      17.68;  Score 572.8;  DB 4;  Length 1626;
Best Local Similarity  61.88;
Matches 1034;  Conservative 0;  Mismatches 547;  Indels 93;  Gaps 4;

Qy      1 ATGCCGGCCATGCGGGGCCTCGGGCGCCTCAGAACACTTCCTGACACCATCGCTACG      60
          ||||||| ||| |||||| |  | || ||||||| |  ||||||||||||||||| ::
Db      1 ATGCCGGTTATGAAAGGATTACTGGCGCGCAAAACACCTTCCTGGACACCATCGCCACC      60

Qy     61 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGCCCAGTGTGGGGGCCTTTC     120
          |||||||| |||| |  |   | |||| ||| |||||||||||||| ||||||| |||
Db     61 CGTTTTGACGGAACACATAGCCAACTTCATCCTTGCCAATGCCCAGTGGCTAAGGGTTTC     120

Qy    121 CCCGTGGTCTACTGCTCTGTG:GACCTCACGGCGTTCTCCCGGGCTGAGGTC         180
          ||| ||  | |||||||||| |   |   | ||| |  ||||||  ||| ||||
Db    121 CCCATAGTCTACTGTTCCGATGGCTTCGCGAGCTTGCTGGA:TTGCCGAACTGAAG:C     180

Qy    181 ATGCAGCGGGC:GTGCC:GTCCC:GCTCCTTATGGGCCAGACCACCAGTGAGCGTCGTCCGC     240
          |||||| || |  | ||| | | ||||||  |||| ||   | | | | ||  ||| ||||
Db    181 ATGACAGAAGAGTTGTAGCTGCAAGTTCTTATTTGGGGTTGAAACCAATGAGCAACTGATG     240

Qy    241 CAACAGATCCGCAAGGGCCTGGACGAGCACCAAGGAGTTCAAGGCTGAGTCCTGAC     300
          ||||| |||| |||||  |  |  | || | ||||||| |||||||| ||| || ||
Db    241 CTTCAAATAGAAAAAGTCACTGGAGGAGAATTCAAAGGAGAATTATGTCTAC      300

Qy    301 CGGAAGAGCGGGC:CCCG:CTGGTGTCTGCTGGAJGTGATACCCATAAAGAATGAGAAA     360
          ||||| || || || ||||   ||| ||  ||| |  |  |||||||||||| | |
Db    301 AAGAAAAACGGGTCTCCATTTGCTGCTGGTTCGTCCCATAAGAATGAAAA     360

Qy    361 GGGGAGGTGGCTGGTCTCTTCTCTCAGTC:CTCACAAGGACAICAGCGAAACCAAGAACCAGAGGG     420
          ||||| | || |  | | ||   |||| || ||| | || | |||||||  |  | ||| ||
Db    361 GGAGATGTAGTACTTTTTTCTCGGCCTCGTTCAAAGATAATAACAGATA-CAAAAG:GAAGAT     419

Qy    421 GGCCCCGACAGA:GGAACGAGCAGAGG:TGGTGGCCGCCGCGIATATGTCGGCGGATCC     480
          |||  |    |  |  |  ||||||||| || |     |   | || |  | |  |
Db    420 TACTTCAGAGAGATAAAAAAGAGACAAAGTCAAAGGAAGAATCAAAGGAGCAGGGACCCA-     475

Qy    481 AAAGGCTTCAATGCCAACCGGCCGGAGCCCGTGCTCTCACCGTGTCCGGCAC     540
          |    ||||||| | | | |    | || ||| || |||| ||||  |||||
Db    477 ----CTTTGACTCAGCCGGAGACGGAGTCGAGCAGTCGAGCAGTGTCACAICACATCCTGGGCAC     531

Qy    541 CTGCAGAAGCAGCCCAAGGGACCAAGGCACACAGTCAATAAAGGGGTGTTTGGGGAGAAACCA     600
          ||| ||||||||   |||  | |  |||  || || | |||||| | ||   ||||| ||
Db    532 CTGCAAAGAAGAGAGAAAGAACAAATTGAAAATAAACAATGTTTTTTGTAGATAATAAACCA     591

Qy    601 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCGTTGCACTCT     660
          ||||| |||| | | |  |  ||||   | |   |||  | || ||  ||||  |||| |
Db    592 GCAATTCCGGAGTATAAAGTTTCTGATGCAGAAAAAGTCCAAATTCATACACTCTCGCATTTT     651

Qy    661 GGGGCACTGAGAGCCACCTGGATGGCTTCATCCTCGCCACACTCTATGTGGCCGTC     720
          ||||| || |  || | | ||  ||   ||| | |||| |  |||  ||  | | |
Db    652 AGCACGCTTTAAAGCTGGCTGGCGGACTGGCTTATTTTGTTGGCAACGTTTTATGTTGCGTG     711

Qy    721 ACTGTGCCTACAGCGTGTGTGAGCACAGCACGGACACCCAGTGCCGCCCGGCCG     780
          |||||||||||||| ||| |||   |  | ||||||| | ||  |  |  || ||
Db    712 ACTGTACCTTACAACGTTTGCTTTATTGGCAATGACGACCTGTCCAACTGGAGC--     768

Qy    781 CCCAGGCTGTCTGTGACCTGGCCGTGGGTGGAGGTCCTTCATCCTTGACATTGTGCTGAATTTC     840
          ||| |  | ||||| ||||||||||  | | |  | | || ||||||  |  || | ||| |||
Db    769 ACAACCTCAGTGACATTGCAGTGCAGTTACTCTTTATTATAGATATTATTTTAAATTTC     828

Qy    841 CGTACCACATTCGTCGTGTCCAGTGCTCGGGCCAGGTGGGTCCAAGTCCCCCAAATGCCTTGCCTC     900
          || ||||||  |  | | | ||||| | ||  ||  | ||| | ||| |||  || |   | |  |
Db    829 CGAACAACTTATGTCAGCAAGTCTGCGGCAAGTAACATTTGCATCCAGCGTGGTGGTGATC     888

Qy    901 CACTACGTCACCACCTGGTTCCTCTGCTGGAJGTCCATCGCCGAJGTGCTGGATGTCATCGCGCTA     960
          |||||| |||||||||||||| ||  |||| |  ||  |  ||| || ||  || | | | ||||
Db    889 CACTATGTCACCACCTGGTTCATCATTGATTAATGCTGCCCGCCTTTGATCTCTG      948

Qy    961 CATGCCGTTCAAGGTCAAGCTGTACTTCGGGGCCAICTGCTGCATCTCTGGAGACGGGCCGCTG    1020
          |||||  | |||  |  |  || || |  || || |   |  |  |||| |||||  |  ||||
Db    949 ?ATGCTTTCAAGTCACAGTGGTGTTCTGTGCATCTTCTAAAGACAGTGCGGCCTCGTG    1008

Qy   1021 CGCCTGCTGCGCCTGCTTCCGGCCCGGAJCGCCCGGCC:GGACCGGTACTTCGCAG?ACAGCGCGCTGGTTGCTG    1080
          |||||| |  |||| || |||| ||| |   || |||  |||| ||  | |||    | ||   || || |  |||
Db   1009 CGTCTTTTGCGTCTGCTGCGAGAAGTTAGACCGCTATTCCAACACCAGTACTATCGTCCTG    1068

Qy   1081 ACACTGCTCATGGCCGTGTTCGCCCTGCTCCGCCGCACTGGGTGCTGCGTCTGGTTTTAC    1140
          |||| | | |  | | |||| |   ||||  |   || ||  ||| ||  |  ||| |
Db   1069 ACTCTGCTCATGTTTGCACTCTTGCACTTGCACACTGCATGGAT?CTGGTGTAGGTC    1128

Qy   1141 ATTGGCACGCGGAGATGAGAGCAGCGAATCCGACGIGCTGAGATTGGCTGCGCGCAG    1200
          |||||| |  || | | || | |  |  |||  ||||  | |  ||||| ||| |
Db   1129 AATTGGAAAAATGGAGAGGGAAGACAACAGCCTTCTGAAGTGGCAAGTCGGTTGCTTCAT    1188

Qy   1201 GAGCTGGCCGGCCGCCGGGAGACTCCTGGAGCTTCCCGAGGCCTGAGGTC    1260
          || | |  |||  | | || |  |  ||  || ||  | |||||
Db   1189 GAGTTGGGAAAGAGACTGGAATCTCCAIACTA-------------------    1220

Qy   1261 AACAGCTCCGCAGAGTGACAACTGCAGCAGCAGCAACTGCAGAGCGAGGCCAACGGACGGGGGGCTG    1320
          | | ||  | |  | || |  | | || | | ||  |  | | || |  |   |  || |
Db   1221 ------------------------------------------TGGCAAC-    1227

Qy   1321 GAGCTGGTGGGGCCCCGGTGCC?GCCGGCAGCGCC:ACATCACCTCCCTCTACTTCGCCACTC    1380
          ||||||||| |||| | | ||  || ||| | |  ||| | | || | |||| ||  ||||
Db   1228 AATACCTTGGGGGGCCCCCGTCGAJCCGAAGTGCCTAJATGCCGCTCJGTGTACTTCACGCTG    1287

Qy   1381 AGCAGCCTCACCAGCGGTGCGTTCGGCTTGCAACGTGTCCCGCAACGCGGACACCGAGAGATC    1440
          |||||| || ||  |  | || | | ||   || | || |  ||  |  | || | ||  |||
Db   :288 AGCAGCCTCACCAGCGTGGGAACGTCTCTGTTTGGGAACGCCAGAAAAGAT:    1347

Qy   1441 ?TCTCCATCTGCACCATGTCTCAT:GGCGCCTCGATGCAGCCIGGTGGTTTGGGAACGTG    1500
          | || ||||  ||| ||||| ||  ||| ||  || | || | |  |   |||| |  |||
Db   1348 ?TCTCCATCTGCACCATGTCT:TTCCATGCTGTTGGTGCTTGAGCACCGTTGGTGGTGTGAAAACGTG    1407

Qy   :501 ACGGCCACATCAGCGCCATGTACGCCGCGCCGCTTTCIGTACCACAGCGCCACCGCGAC    1560
          || |  | | |  | || | || ||  | | |  | |   || || ||  | || ||
Db   :408 ACACCAATCATACAGACGGATGCTGTACTCCCTA:CACAGAACTAAGGAT    1467

Qy   1561 CTGCGGACTACA?CCGCAT?CCGATCCCCATGCTGGAG    1620
          || |||| |||  || |  |||  |  || | |||| |
Db   1468 CTGAAAGATTCATCCGIGCCATCACTTGCCCAACAACTCAGCGAGGATGCTCGAA    1527

Qy   :621 TACTTCCAGGCCACCTGGGCGGTGAACAATGCATGCACCACCGAGCTGCTG    :674
          |  | ||  | | |  |  ||||  |  | | |  |   | || || |
Db   1528 TATTTTCAAACAACCTGGTCAGTCAACAATGGAATAGATTCAAATGAGGTAATG    1581
```

US-09-358-383C-4

Query Match   17.6%;   Score 572.8; DB 4;   Length: 2694;
Best Local Similarity   61.8%;   Pred. No. 2.3e-111;
Matches 1034;   Conservative   0; Mismatches 547;   Indels   93; Gaps   4;

RESULT 15
US-09-358-383C-14
; Sequence 14, Application US/09358383C
; Patent No. 6518398
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/09/358,383C
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 5955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (196)..(1770)
; NAME/KEY: intron
; LOCATION: (1771)..(2618)
; NAME/KEY: exon
; LOCATION: (2619)..(4364)
; OTHER INFORMATION: At position 5625, n=any nucleic acid
US-09-358-383C-14

Query Match   17.6%;   Score 572.8;   DB 4;   Length 5955;
Best Local Similarity   61.8%;   Pred. No. 2.9e-111;
Matches 1034;   Conservative   0;   Mismatches 547;   Indels   93;   Gaps   4;

```
Qy      1 ATGCCGGCCATGCGGGGCCTCCTGCGCCTCGAGAACACCTTCCTGACACCATCGCCTACG   60
            ||||||||||||| ||||||||| || ||| |||| || |||   |||||||| ||||||
Db    196 ATGCCGGTTATGAAAGGATTACTGCGCCCGCAAAACACCTTCCTGGACACCACCGCCACC  255

Qy     61 CGCTTCGACGGCACGCACGTAACTTCGTTCTGGGCAACGCCCAGGTGGCGGGGGGCTCTTC  120
            |||| || |||||| ||||  || ||||||||||  |||||||||||| |||||||
Db    256 CGTTTGACGGAACACATAGCCAATCCATCCTTGCCAATGCCCAGGTGGCTAAGGGTTTC   315

Qy    121 CCCGTGGTCTACTCCTGTGATGGCTTCTGCCAGCGGTTCTCCCGGGCTGAGGTC         180
            ||| ||||||||||||| ||||||  || |||||||  |||  |||||||||||
Db    316 CCCATAGTCTACTGTTCCGATGGCTTCTGCGAGCTTGCTGGATTGCCCGAACTGAAGTC   375

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Search completed: October   1, 2003, 21:16:56
Job time : 231 secs

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                    GenCore version: 5.1.6
            Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw mode.

Run on:    October  1, 2003, 19:33:31 ; Search time 788 seconds
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Perfect score:  3252
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Scoring table:  IDENTITY_NUC
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Searched:       1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters:    3416838

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3245.8	99.8	3249	14	US-10-160-224-2		Sequence 2, Appli
3	3218	99.0	3857	14	US-10-121-746-19		Sequence 19, Appli
4	3156	97.0	3355	9	US-09-119-855-1		Sequence 1, Appli
5	3156	97.0	3355	14	US-10-185-867-1		Sequence 1, Appli
6	3153	97.0	3249	14	US-10-185-867-3		Sequence 3, Appli
7	3144	96.7	3240	9	US-09-119-855-3		Sequence 3, Appli
8	2664.8	81.9	3715	10	US-09-965-830-9		Sequence 9, Appli
9	884.8	27.2	3064	10	US-09-965-830-5		Sequence 5, Appli
10	869.8	26.7	3736	10	US-09-965-830-10		Sequence 10, Appli
11	844.4	26.0	870	9	US-09-119-855-9		Sequence 9, Appli
12	844.4	26.0	870	14	US-10-185-867-9		Sequence 9, Appli
13	844.4	26.0	1132	9	US-09-119-855-7		Sequence 7, Appli
14	844.4	26.0	1132	14	US-10-185-867-7		Sequence 7, Appli
15	761.2	23.4	3321	14	US-10-185-867-17		Sequence 17, Appli
16	761.2	23.4	5107	14	US-10-185-867-15		Sequence 15, Appli
17	572.8	17.6	1626	9	US-09-119-855-6		Sequence 6, Appli
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28	361.6	11.1	3041	14	US-10-188-341-19		Sequence 19, Appli
29	361.6	11.1	3041	14	US-10-188-297-19		Sequence 19, Appli
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ALIGNMENTS

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RESULT 1
US-09-965-830-1
; Sequence 1, Application US/09965830
; Patent No. US2002017201A1
; GENERAL INFORMATION:
;  APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
;  TITLE OF INVENTION: A novel potassium channel protein
;  FILE REFERENCE: Y9903-PCT
;  CURRENT APPLICATION NUMBER: US/09/965,830
;  CURRENT FILING DATE: 2001-10-01
;  PRIOR APPLICATION NUMBER: 09/600,776
;  PRIOR FILING DATE: 2001-07-21
;  PRIOR APPLICATION NUMBER: JP P1998-346198
;  PRIOR FILING DATE: 1998-12-04
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;  LENGTH: 3323
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (6)..(3257)
US-09-965-830-1

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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 3252;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; TITLE OF INVENTION: Human Elk, a Voltage-Gated Potassium Channel Subunit
; FILE REFERENCE: 018512-0013200US
; CURRENT APPLICATION NUMBER: US/10/160,224
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: US/09/343,494
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
; LENGTH: 3249
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3249)
; OTHER INFORMATION: hElk
US-10-160-224-2

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Db   2886 TGGCCCACCCTCGTCCGGGGCCTCCTCTGCTCTGCACCCTGGGCCTGGGGTCCCCA 2945

Qy   2941 GCGTCTCAGAGCTCCCCCTGGCCCCGCCCAGAGCCCACAGCTTCTGGACCTCACCTCAGACTCA 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2946 GCGTCTCAGAGCTCCCCCTGGCCCCGCCCAGAGCCCACAGCTTCTGGACCTCACCTCAGACTCA 3005

Qy   3001 GAGCCCCGCCCTGCTCGCTCTGCTCTTGAGCCCAGCACCCCTGCCCCTCCCTCCCTCCT 3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3006 GAGCCCCGCCCTGCTCGCTCTGCTCTTGAGCCCAGCACCCCTGCCCCTCCCTCCCTCCT 3065

Qy   3061 TCTGAGGAAGGGCTCAGAGCTGCGGCCCCGAGAGCCTGTGAGCCTGAGCCAGCTACCAGC 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3066 TCTGAGGAAGGGCTCAGAGCTGCGGCCCCGAGAGCCTGTGAGCCTGAGCCAGCTACCAGC 3125

Qy   3121 ACTGGAGAGCCCCCCACCAGGGTCAGGGGCTCAGGGCCATGCCTCGGCACAGCCCCACAGCCTG 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3126 ACTGGAGAGCCCCCCACCAGGGTCAGGGGCTCAGGGCCATGCCTCGGCACAGCCCCACAGCCTG 3185

Qy   3181 GAGATGTGCTTATTGGCTGCCATGGCTCCTGCCACAGTCCAGTGACCCAGGAAGAAGGC 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3186 GAGATGTGCTTATTGGCTGCCATGGCTCCTGCCACAGTCCAGTGACCCAGGAAGAAGAGGC 3245

Qy   3241 ACAGGGTCTGA 3252
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Db   3246 ACAGGGTCTGA 3257
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RESULT 2
US-10-160-224-2
; Sequence 2, Application US/10160224
; Publication No. US20030077731A1
; GENERAL INFORMATION:
; APPLICANT: Jegla, Timothy J.
; APPLICANT: Wickenden, Alan
; APPLICANT: ICAgen, Incorporated
```

(DNA sequence alignment, two sequences labeled Qy and Db, positions 781–3000)

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Db  2941  GGGTCTCAGAGCTCCCCCGCTGCCTCGAGCCACAGTTCTGGACCTCCACCTCAGACTCA  3000
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Qy  3001  GAGCCCCTGCCTCAGGAGACCTCTGCTCGTCGAGCCCAGCACCCCTGCCTCCCTCCTCCTT  3060
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db  3001  GAGCCCCTGCCTCAGGAGACCTCTGCTCGTCGAGCCCAGCACCCCTGCCTCCCTCCTCCTT  3060

Qy  3061  TCTGAGGAAGGGGCTAGGACTGGGCCCCGCAGAGCCTGTGAGCCAGGCTACCCAGG  3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  ACTGGGAGCGGGCCCCACCAGGGTCAGGGGGCCTGGCCTGGGACCCCCACAGCCTG  3120

Qy  3121  ACTGGGAGCGGGCCCCACCAGGGTCAGGGGGCCTGGCCTGGGACCCCCACAGCCTG  3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  GAGATGTGCTTATTGGCTGCCATGGCTGCCATGGGCCACAGTGCCACAGTGCCACAGT  3240

Qy  3181  GAGATGTGCTTATTGGCTGCCATGGCTGCCATGGGC  3240
          |||||||||||

Qy  3241  ACAGGGGTC  3249
          |||||||||
Db  3241  ACAGGGGTC  3249
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RESULT 3
US-10-121-746-19
; Sequence 19, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:
;   APPLICANT: Miller, Andrew P.
;   APPLICANT: Curran, Mark Edward
;   APPLICANT: Hu, Ping
;   APPLICANT: Rutter, Marc
;   APPLICANT: Wang, Jian-Wang
;   TITLE OF INVENTION: No. US20030036648A1e1 Human Potassium Channels
;   FILE REFERENCE: SEQ-15P
;   CURRENT APPLICATION NUMBER: US/10/121,746
;   CURRENT FILING DATE: 2002-04-11
;   PRIOR APPLICATION NUMBER: US/09/336,643A
;   PRIOR FILING DATE: 1999-06-18
;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
;   PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
;   PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
;   PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
;   PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
;   NUMBER OF SEQ ID NOS: 87
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 3857
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (249)...(3495)
;   OTHER INFORMATION: K+Hnov14
US-10-121-746-19

Query Match   99.0%; Score 3218; DB 14; Length 3857;
Best Local Similarity   99.8%;
Matches 3244; Conservative 0; Mismatches 0; Indels 5; Gaps 2; Pred. No. 0;

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Qy     1  ATGGCCGGCCATGCGGGGCGCTCCTGCGCGCTCAGAACACCTTCCTGGACACCATCGCTACG   60
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   249  ATGGCCGGCCATGCGGGGCGCTCCTGCGCGCCCGCAGAACACCTTCCTGGACACCATCGCTACG  308

Qy    61  CGCTTCGACGGCACGCACGCCAGTAACTTCGTGCTGGGCAACGTGGCCCAGGTGGCGGGGCTCTTC  120
          |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   309  CGCTTCGACGGCACGCACGCCAGTAACTTCGTGCTGGGCAACGTGGCCCAGGTGGCGGGGCTCTTC  365

Qy   121  CCCGTGGTCTACTGCTCTGATGGCTTCTCTGACCTTCACGGGCTTCTCCCGGCTGAGGTC  180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   366  CCCGTGGTCTACTGCTCTGATGGCTTCTCTGACCTTCACGGGCTTCTCCCGGCTGAGGTC  425
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(DNA sequence alignment — Query "Qy" vs Database "Db" rows, middle and right columns)

RESULT 4
US-09-119-855-1
; Sequence 1, Application US/09119855
; Patent No. US20020099197A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: mni-055
; CURRENT APPLICATION NUMBER: US/09/119,855

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; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 1
;   LENGTH: 3355
;   TYPE: DNA
;   ORGANISM: Monkey
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (113)..(3352)
US-09-119-855-1
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Query Match         97.0%;    Score 3156;   DB 9;   Length 3355;
Best Local Similarity  98.2%;  Pred. No. 0;
Matches 3192;    Conservative  0;   Mismatches  60;   Indels  0;   Gaps  0;
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Qy     1 ATGGCGGCCATGGGGCGGGGCCTCCTGGGGCCTCAGAACACCTTCCTGGACAACACCTCACC 60
           ||||||||||||||||||||||||||||||||||||||||||||||| |||||||:||||
Db   104 ATGGCGGCCATGGGGCGGGGCCTCCTGGGCCGCAGAAACACTTCCTGGACACCA-CGCTACG 163

Qy    61 CGCTTCGACGGCACGCACAGTAACTCGTGTCGGCAACGCCCAGCTGGCGGGCTTC 120
           |||||||||||||||||| :||||||||||||||||||||||||||||||||
Db   164 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGCAACGCCCAGCTGGCGGGCTCTTC 223

Qy   121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCACGGGCTTCTCCCGGGCTGAGGTC 180
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   224 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACC-CACGGGCTTCTCCCGGGCTGAGG-C 285

Qy   181 ATGCAGCGGGGCTGTCCCTGCTCCTTCCTTATGGGCCAGAACACCAGTGAGCTCGTCCGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   284 ATGCAGCGGGGCTGTGCCCTGCTCCTTCCTTATGGGCCAGAACACCAGTGAGCTCGTCCGC 343

Qy   241 CAACGATCCGACAAGGCCTGAGAGCGACACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300
           ||||||||||||||||||||||| :|||||||||||:||||||||||||||||| ||||
Db   344 CAACAGATCCGACAAGGCCCACGACGCGAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 403

Qy   301 CGGAAGAGCGGGGCTCCCGTTCTGTGTCTCTGGATGTGATACCCATAAAGAAGAATGAGAAA 360
           |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   404 CGGAAGAGCGGGGCTCCCGTTCTGTGTCTCCTGGATGTGATGATACCCATAAAGAAGAATGAGAAA 453

Qy   361 GGGAGGTGGCTCTCTTCCACAAGGACATCAGTGGTGGCGGCGGCGGCGGCAGCCGCACGCGCGGAGG 420
           |||||||||||| |||||||||||||||||| :|||||||||||||||||||||||
Db   464 GGGAGGTGGCTCTCTTCCTCACAAGGACACAGTGAAACCAAGGCACCAAGAACCGGAGGG 523

Qy   421 GGCCCCGACAGATGGAAGGAGAGACCAGGGGTGGTGGCCGGCGGCCGGCCGTCTCCGGGCACGATCC 480
           |||||| ||||||||||||||| |||||||||||||||||||||| |||||
Db   524 GGCCCTGACAGATGGAAGGAGAGCCAGGTGGCCGGCGGCCGGCCGATGGCCGGCGGCCGATCC 583

Qy   481 AAAGGCTTCAATGCCAACCGGGAGCGGGCAAGCACAAGCTCAATAGGGGGGTGTTGGGGAGAAACCA 540
           ||||||||||||||||||||||||||| ||||||||||||||||| ||||||||||||
Db   584 AAAGGCTTCAATGCCAACCGGGAGCGGGCCAAGCACCACAAGCTCAATAGGGGGGTGTTTGGGGGAGAGCCA 643

Qy   541 CTGCAGAAGCAAGCCCAAGGCAAGCACAGCAGCAAGGCTTCATCCGGAAGTCGCCTTCATCCGCCACT-GTGCTGTC 600
           ||||||||||||| :|||||||||||||||||||| ||||||||||||||||||| ||||
Db   644 CTGCAGAAGCAAGCCCAACCGGGAGCGGGCCAGCACCAAGCTCAATAGGGGGGTGTTTGGGGGAGAGCAGCCA 703

Qy   601 AACTTGCCTGAGTAGTAGAAAGTAGCCGCATTACTGCCGCTTCATCATCCGGATGCCGCACTGT 660
           |||||||||||||||| || ||||||||| |:||||||||||||||||||||
Db   704 AACTTGCCTGAGTAGTAGAAAGTAGCCGCATTACTGCCGCTTCATCATCCGGATGCCGCACTGT 763

Qy   661 GGGGCACTGAGAGCACCTGGATGGCTTCATCATCCGCTGCCGCTAGTGTGGCTGTC 720
           |||| ||||||||||||||||||||||||||||||||| |||||||||||||||
Db   764 GGGGCGCTGAGAGCACCTGGATGGCTTCATCATCCGCTGCCGCCTATGTGGCTGTC 823

Qy   721 ACTGTGCCCTACAGCGTGTGTGAGCAGCACACGGGGAGCTCTTCATCCTTGACATTGTGCTGAATTTC 780
           || |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db   824 ACCGTGCCCTACAGCGTGTGTGAGCAGCACACGGGGAGCTCTTCATCCTTGACATTGTGCTGAATTTC 883

Qy   781 CCCAGCGTCTGTGACCTGGCCCAGGTGGTTGCTCTGGAGGTCTTCATCCTTGACATTGTGCTGAATTTC 840
           |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db   884 CCCAGCGTCTGTGACCTGGCCCAGGTGGTTGCTCTGGAGGTGCTCAAGGTTGCTGCCTCTAGGG 943

Qy   841 CGTACCACATTCGTGTCCAAGTCGGGCCCAGGTGGTGTTTGCCCCAAAGTCCATTTGCCTC 900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   944 CGTACCACATTCGTGTCCAAGTCGGGCCCAGGTGGTGTTTGCCCCAAAGTCCATTTGCCTC 1003
           |||||||||||||||||||||||||||||||||||||||||||||||
Qy   901 CACTAGTCACCACCTGTTCCTGCTGGATGTCATCGCAGGCCATGCGAGG 960

Db  1004 CACTAGTCACCACCTGTTCCTGCTGGATGTCATCGCAGCGCTGCCTGCTG 1063
           ||||||||||||||||||||||||||||||||
Qy   961 CATGGCCTTCAAGTCAACGTGTACTTCGGGGCCCATCTGCTGGGACGTGCCGCTGCTG 1020

Db  1064 CATGGCCTTCAAGTCAACGTGTACTTCGGGGCCCCACTGCTGGGACGTGCTGCTG 1123
           |||||||||||||||||||||||||||| ||||||||||||||||||
Qy  1021 CGCCTGCTGCCGCCGCTTCCCGGCCGGCTGGACCGGTACTCCAGTACGCACCGGCCGGTCGG 1080

Db  1124 CGCCTGCTGCTGCCGCTTCCCGGCCTGGCTGGACTACTCCAGTACGCACCGGCCGGTCGG 1183
           ||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1081 ACACTGCTCATGGCCGTGTTCGCCCTGCTCGGCACTGGTCTCGGTGTTTAC 1140

Db  1184 ACACTGCTCATGGCCGTGTTGCCCTGTTGCCCACTGGTCTCGGTCGTGTTTAC 1243
           |||||||||||||||||||||||||||| |||||||||||||| |||||
Qy  1141 ATTGGCAGCGGGAGATCCAGAGCAGCGAATCCAGCCTGCGAGATTGGCTGCTCGCAG 1200

Db  1244 ATTGGTCACGGGAGATCGAGACAGCAGGCAATCCCAGCCTGCGAGATTGGCTGCTCGCAG 1303
           ||||| ||||||||| ||| |||| ||| ||||||||||||||||||||||
Qy  1201 GAGCTGGCCGGCCGACTGGAGACTCCCTACCTTGGTGGGCGCAGCCAGCCGAGGG 1260

Db  1304 GAGCTGGCCGGCCGACTGGAGACTGGAGCGCCCCTACTTGGTGGGCGCAGCCAGCCGAGGG 1363
           |||||||||||||||||||||| |:||||| ||||||||||||||||||||||
Qy  1261 AACAGTTCCGGCCAGAGTGACAACTGCAGCAGCAGGAGGCAGCAACGGGACGGGGGGCTG 1320

Db  1364 AACAGCTCTGGCCAGAGTGACAACTGCAGCAGCAGGAGGCAGCAACGGGGACGGGGGCTG 1423
           ||||| |||||||||||||||||||||||||||||||||||||||| |||||||
Qy  1321 GAGCTGTGTGGGCGGCTGCATGTCTCATCCTGCAGGCCTCACATCCCCTCTACTTCGCACTC 1380

Db  1424 GAGCTGTAGGGCGGCTGCATGTCTCATCCTGCAGGCCTCACATCCCCTCTACTTCGCACTC 1483
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1381 AGCAGCCTCACAGCGGTGCCAACGTGTCCGCAACGGTGTCCGGCCACAGCCGCACGCGCGACC 1440

Db  1484 AGCAGCCTCACAGCGGTGCCAACGTGTCCGCAACGGTGTTCTGTACCACGCGCACGCGCGAC 1543
           ||||||||||||||||||||||||||||||||||||| |||||| ||||||||||||
Qy  1441 TTCTCCATCTGCACCATGTCTATCGCCGGATCCGGATCCGCGATATCCGGATCCTCAAGCCCTATCCCCGCACTC 1500

Db  1544 TTCTCCATCTGCACCATGTCTATCGCCGGATCCGGATCCGCGATATCCGGATCCTCAAGCCCTATCCCCGCACTC 1603
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Qy  1501 ACGGCCATCATCCACGCGATGTGACGTGCCCGCCTTCGTGTACCACGCGCACGCGCGAC 1560

Db  1604 ACGGCCCATCATCCACGCGATGTGACGTGCCCGCCTTTGTGTTGCGGGACGCGCACGCGCGAC 1663
           ||||| ||||||||||||||||||||||||||| |||||||| |||||||||||||
Qy  1561 CTGCGGCGACTACATCCGGCATCCGCATCCGGATCCTCAAGCAGCCCCTATCCCCGCTGCTGGAG 1620

Db  1664 CTGCGGCGACTACATCCGGCATCCGGCATCCGGATCCTCAAGCAGCCCCTATCCCCGCTGCTGGAG 1723
           |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Qy  1621 TACTTCCAGGCACTGGGCGGCGTGAACAATGGCCATGCGACACCTGACACCGAGCGTCTGCAGCTG 1680

Db  1724 TACTTCCAGGCACTGGGCGGCGTGAACAATGGCCATGCGACACCTGACACCGAGCGTCTGCAGCTG 1783
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1681 CTCCCTGACGAGCTGTGAGGCGAGAGCAGCTGCCATGCGCCATGCCCATCCACAAGAGGTCTGCAGCTG 1740

Db  1784 CTCCCTGTTGAGGCGAGAGCAGCTGCCATGCGCCATGCCCATCCACAAGAGGTCTGCAGCTG 1843
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1741 CCACTGTTGAGGCGAGAGCAGCTGCCTGCCTGCCGCTCTGGCGCTGCTGCGGGCCC 1800

Db  1844 CCGCTGTTGAGGCGAGAGCAGCTGCCGCTGCCTGCCCGCTCTGCGGGCCC 1903
           || |||||||||||||||||||||| |||||||||||||||||||||||||
Qy  1801 GCCTTCTGCACGCCGGGGAGTACCTCATCATCCACAAGGCGATGCGGCACCGCCCTCTAC 1860

Db  1904 GCCTTCTGCACGCCGGGGAGTACCTCATCATCCACAAGGCGATGCGGCACCCCTCTAC 1963
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1861 TTTGTCTGCTCTGGCTCTGGCTCCATGGAGGTGCTCCAAGGTGGCACCGTGCTCGCCAAGGCCAATGCC 1920

Db  1964 TTTGTCTGCTCTGGCTCTGGCTCCATGGAGGTGCTCCAAGGTGGCACCGTGCAGGCCAATGCC 2023
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1921 AAGGGCGACCTGATCGGCTGTGAGCTGCCCGGCGGAGCAGGTGGTAAAGGCCAAGCC 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  2024  AAGGTGACCTGATCGGCTGCTGAGCTGCCCCGGAGGGAGCAGGTGGTAAAGGCCAAGCGGC    2083
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Qy  1981  GACGTGAAGGGGCTGACGTACTGCGGTCCTGCAGTGTCTGCAGCCTGGCCTGGCTGCACGAC    2040
                |||||||||||||| ||||||||||||||||||| ||||||||||||||||||||||
Db  2084  GATGTGAAGGGGCTGACGTACTGCGGTCTGCAGTGTCTGCAGCCTGGCCTGGCTGCACGAC    2143
Qy  2041  AGCCTTGCGCGTCTACCCCGAGTTGCCCGGCTTGCCCCGCGAGTGGCTGTCGAGGGGAGCTC    2100
Db  2144  AGCCTTGCGCTCTACCCCGAGTTGCCCGGCTTGCCCCGCGAGTGGCTGTCGAGGGGAGCTC    2203
Qy  2101  AGTTACAACCTGGGTGCTGGGGAGCTTCTCGAGAGTGGACACCACTCCCTGAGCGGC      2160
Db  2204  AGTTACAACCTGGGTGCTGGGGAGCTTCTCGAGAGTGGACACCACTCCCTGAGCGGC      2263
Qy  2161  GACAAATACCCTTATGTCCACGCTGGAGGAGGAGGACAGATGGGGAGCAGGGCCCACG     2220
Db  2264  GACAATACCCTTATGTCCACGCTGGAGGAGGAGGACAGATGGGGAGCAGGGCCCACA      2323
Qy  2221  GTCTCCCCAGCCCAGCTGATGAGCCCTCCAGCCCCCTGCTGTCCCCGTGGCTGCACCTCC    2280
Db  2324  GTCTCCCCAGCCCAGCTGATGAGCCCTCCAGCCCCCTACTGTCCCCGTGGCTGCACCTCT    2383
Qy  2281  TCATCCTCCGCTGCCAAGCTGCTATCCCCACGTGCGAACAGCACCCCGGCCTCGTCTAGGT    2340
Db  2384  TCATCCTCGGCTGCCAAGCTGTCTATCCCCACGTGCGAACAGCACCCCGGCCTCGTCTAGGT    2443
Qy  2341  GGCAGAGGGAGGCCAGGCAGGCGCTTGAAGGCTGAGGCTGGCCCCTCTGCTCCC         2400
Db  2444  GGCAGAGGAGGACCAGGCAGGGCGCTTGAAGGCTGAGGCTGGCCCCTCTGCTCCC        2503
Qy  2401  CCACGGGCCTAGAGGGGCTACGGCTGCCCCCATGCCATGCCCCCAGATCTG           2460
Db  2504  CCACGGGCCTAGAGGGGCTACGGCGTGCCCCCATGCCATGCCCCCAGATCTG          2563
Qy  2461  AGCCCCAGGGTAGTAGATAGATGGCATTGAAGACACGGCTGTGGTCGGACCAGCCAAGTTCT    2520
Db  2564  AGCCCCAGGGTAGTAGATAGATGGCATTGAAGACACGGCTGTGGTCGGACCAGCCAAGTTCT    2623
Qy  2521  TTCCGGCTGCTGGCCCAGTCTGGCCCGGAATGTAGCAGCAGCCCCCTCCCCCTGGACCAGAGCC    2580
Db  2624  TTCCGCATGGCCCGGAATGTAGCCCGGAATGTAGCAGCAGCCCCCTCCCCCTGGACCAGAGT    2683
Qy  2581  GGCCTGCTCACTGTCCCCCA·GGGCCCAGGGAGGAACAGGAAGGAACACAGACCACTGGACAAG    2640
Db  2684  GGCCTGCTCACTGTCCCCCATGCCCCAGGGAGGAACAGGAAGGAACACAGACCACTGGACAAG    2743
Qy  2641  CTTCGGCAGGCGGTGACAGAGCTGTGTCAGAGAGCAGTGCTGCAGAATGCGGGAAGGACTGCAG    2700
Db  2744  CTTCGGCAGGCGGTGATGGAGCTGTGTCAGAGAGCAGTGCTGCAGAATGCGGGAAGGACTACAG    2803
Qy  2701  TCACTTCGGCAGGCGTGTGCAGCTTGTCTGCAGCTTGTCGGGGAGGGTCCGTGCCCTCGG     2760
Db  2804  TCACTTCGGCAGGCTGTGCAGCTTGTCCTGCGGCACCCATGGGAGGGGCCATGCCCTCGG    2863
Qy  2761  GCATCGGGGAGAGGGCCGTTCCCGGGCTCCCAGCCACACCTCCTGTGGTGTCG·TGTGGTG·     2820
Db  2864  GCCTCAGGAGGGGCCGCCATGCCCCAGCTTCCGGGCTTCTCCAGCCTCTGTGTCGGTG      2923
Qy  2821  GACACTGGGGCATCCTCCTACTGCGCTTCAGCCCCTGGCTCTGTCTGTTGAGTGGGGACT     2880
Db  2924  GACACTGGGGCATCCTCCTACTGCCTCTGCCTGCCCCTGGCTCTGTCTGTTGAGTGGGGACT    2983
Qy  2881  TGGCCCCACCCGTCGGGGGCCTCTCCCCCTCATGGCACCCTGGCCTCGGGGTCCCCCA      2940
Db  2984  TGGCCCCACCCGTCGGGGGCCTCTCCCCCTCATGGCACCCTGGCCTCGGGGTCCCCCA     3043
Qy  2941  GGGCTCTCAGAGCTCCCCTGGACCTCGACGTTCTCCACCTCCACACTCA              3000
Db  3044  GCATCTCAGAGCTCAGAGCCTTTCTGGACCTCCACCTCCACCTCAGACTCCA            3103
Qy  3001  GAGCCCCCTGCCTCAGGGAGACCTGCTCTGCTCTGAGCCCTGCCTCCCCT            3060
Db  3104  GAGCCCCCTGCCTCAGGGAGACCTGCTCTGCTCTGAGCCCTGCCTCCCCT           3163
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Db  3061  TCTGAGGAAGGGCTAGGACTGGGGCCCGGAGAGCCTGTGAGGCTGAGGCTGAGGCTGACCAGC    3120
                ||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Qy  3:64  TCTGAGGAAGGGGCTAGGACTGGGGCCCCCCAGAGCCTGTGAGGCTGAGGCTGAGGCTGACCAGC    3223
Qy  3121  ACTGGAGAGCCCCACCAGGTCAGGGGCTCAGGGGCCTGGCCTGCCGGGGGCCCCACCAGCCTG    3180
Db  3224  ACTGGAGAGCCCCACCAGGGTCAGGGGCCCCCAGTGTCAGGGGCCCTGGGGCCCCCACCAGCCCG    3283
Qy  3181  GAGATGGTGCTTATTGGCTGCCATGGCTCTCGGCACAGTCCATGGTGACCCAGGAGGAAGGC    3240
Db  3284  GAGATGGTGCTTATTGGCTGCCACGGCTCTCGGCACAGTCCAGTGCACCCAGGAGGAAGGC    3343
Qy  3241  ACAGGGGTCTGA    3252
                ||||||||||||
Db  3344  ACAGGGGTCTGA    3355
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RESULT 5
US-10-185-867-1

;  Sequence 1, Application US/10185867
;  Publication No. US20030104429A1
;  GENERAL INFORMATION:
;  APPLICANT: Curtis, Rory A.J.
;  TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
;  FILE REFERENCE: MNI-055CP
;  CURRENT APPLICATION NUMBER: US/10/185,867
;  CURRENT FILING DATE: 2002-06-27
;  PRIOR APPLICATION NUMBER: US/09/358,383
;  PRIOR FILING DATE: 1999-07-21
;  PRIOR APPLICATION NUMBER: USSN 09/119,855
;  PRIOR FILING DATE: 1998-07-21
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 1
;    LENGTH: 3355
;    TYPE: DNA
;    ORGANISM: Macaca sp.
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (104)..(3352)
US-10-185-867-1

  Query Match             97.0%;  Score 3156;  DB 14;  Length 3355;
  Best Local Similarity   98.2%;  Pred. No. 0;
  Matches 3192;  Conservative   0;  Mismatches  60;  Indels   0;  Gaps   0;

Qy    1  ATGGCGGCCATGCAGGCGGGGGCCTCTCGGGCCCTCAGAACACTTCCTGGACACCACTTCCTGGACCACCTGCTACG     60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db  164  ATGGCGGCCATGCAGGCGGGGGCCTCCTCCTCGGCCGCGAACACTTCCTGGACCACATGGCTACG    163
Qy   61  CGCTTCGACGGCAGCACGACCAGTAACTTCGTGCTGGGCAACGCCCAGGTGGCGGCGGGCTCTTC    120
            |||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db  164  CGCTTCGACGGCAGCACGACCAGTAACTTCGTGCTGGGCAACGCCCAGGTGGCGGCGGGCTCTTC    223
Qy  121  CCGGTGGTCTACTGCTCGTGATGGCTTCTGTGACTCACGGCGTCTCCCGGCTGAGGTC        180
            ||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db  224  CCGGTGGTCTACTGCTCGTGATGGCTTCTGTGACTCACGGCGTCTCCCGGCTGAGGTC       283
Qy  181  ATGCAGCGGCGGCTGTGCCTGCGGCACCAGCCAGTGAGTCGTCCGGC         240
            ||||||||||||||||||||||||||||||||||||||||||||||
Db  284  ATGCAGCGGCGGCTGTGCCTGCGGCACCAGCCAGTGAGCTGTCGTCCGGC       343
Qy  241  CAACAGATCCGCAAGGCCCTGGACACAAGGAGTTCAAGGTGGGCTGAGTCTGTAC     300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  344  CAACAGATCCGCAAGGCCCTGGACACAAGGAGTTCAAGGTGGGCTGAGTCTGTAC    403
Qy  301  CGGAAGAGCGGGCTCCGTTCCGGGATGTCTCCGTGGTATACCCATGTGATACCCAITGAGAAA    360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  404  CGGAAGAGCGGGCTCCGTTCCGGGACCATCAGGGAGTCAATCAGCGAACCAGGACCGAGGG    463
Qy  361  GGGAGGTGCTGCTCTTCCTCTTCCAGTCTCTCACAAGGACATCAGCGAAACCAGACCGAGGG    420
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Db   464 GGGGAGGTGGCTCTCTTCCCTAGTCTCTCACAAGGACATCAGTGAAACCAGGG 523

Qy   421 GGCCCGACAGATGGAAGGAGACAGGTGTGGCCGGCCGCGATATGGCCGCACGATCC 480
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Db   524 GGCCCTGACAGATGGAAGGAGGAGACAGGTAGTGGCCGGCCGCGATATGGCCGCACGATCC 583

Qy   481 AAAGGCTTCAATGCCAACCGGCGGCGAGCCGGCCGGGCCGGGCCGTCTCTACCACCTGTCGGGCCAC 540
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Db   584 AAAGGCTTCAATGCCAACCGGCGGCGAGCCGGGCCGGGCCGTCTCTACCACCTGTCGGGCCAC 643

Qy   541 CTGCAGAAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTGGGGAGAAAACCA 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   644 CTGCAGAAGCAGCCCAAGGCAAGCAAGCACAAGCTCAATAAGGGGTGTTGGGGAGAAGCCA 703

Qy   601 AACTTGCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTG 660
         ||||||||||||||||||| ||||||||| |||||||||| ||||  ||||||
Db   704 AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT 763

Qy   661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCGCCACACTCTATGTGGCTGTC 720
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Db   764 GGGGCGGCGTGAGGGCCACCTGGGATGGCTTCATCCTGCGCCACATGCTATGTGGCTGTC 823

Qy   721 ACTGTGCCCTACAGCGGTGTGTGTGAGCACAGACACGGTTCCTCTTCATCTTGACATGTGCTGAATT 780
         ||||||||||||||||||| ||||||||||||||||| | |||| ||||||||||
Db   824 ACCGTGCCCTACAGCGGTGTGTGTGAGCACAGGCACGGATGCTCAAGGTGCTCAAGGTGCACCGGTGCTCAAGGTGCACCGTGCCCATCCTAC 893

Qy   781 CCCAGGCTCTGTGACCTGGAGGTCCTCTTCATCTTGACATGTGCTCATTGCCTC 840
         ||||||||||||||||| |||||||||| ||||||||||||||||||||
Db   884 CCCAGGCTCTGTGGACCTGTGGAGGTCCTCTTCATCTTGACATTGCTCATTGCCTC 943

Qy   841 CGTACCACATTCGTCGTGCCCAGGTGGTGTTGCCCCAAAGTCCATTGCCTC 900
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Db   944 CGTACCACATTCGTGTCCCAGGTGGTGTTGCCCCAAAGTCCATTGCCTC 1003

Qy   901 CACTACGTCACCACCTGGTTCCTGCTGGAGTCTACGCCAGTGTCCCCTTGACCTGC-A 960
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Db  1004 CACTACGTCACCACCTGGTTCCTGCTGGATGTCATCGCAGCGCCCAGTGTCCCCTTGACCTGCTG 1063

Qy   961 CATGCCTTCAAGGTCAACGTGTACTTCGGGGCCCATCCTGCTGAAGCGGTGCGCCCTGCTG 1020
         ||||||||||||||||||||| |||||||||||||||||||||| |||||||||||
Db  1064 CATGCCTTCAAGGTCAACGTGTTACTTCGGGGCCCATCCTGCTGAAGACGGTGCCGTTCTG 1123

Qy  1021 CGCCTGCTGCTGCCCTGCTTCGGGCCTGGACCGGTACTCGGACGCGCCGGTGTCTG 1080
         |||||||||||||||||||||||||||||||| |||||||||||||||||||
Db  1124 CGCCTGCTGCTGCCCTGCTTCCGGCCTGGACCGGTACTCGGACGCGCCGGTGTCTG 1183

Qy  1081 ACACTGCTCATGGCCGTGTTCGGGGTGCCCTGCTCGCGGCACTGGGTCGCGTTGGTTTAC 1140
         |||||||||||||||||||||| |||||||||||||||||||||||||||||
Db  1184 ACACTGCTCATGGCCGTGTTGCCCGGGGTGTTCGGGGTGCCCTGCTCGCGGTCTGGTTTAC 1243

Qy  1141 ATTGGCAGCAGCGGGAGATCGAGAGCAGCAATCCGAGATTGGCTGGCTGCAG 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1244 ATTGGTCAGCGGGAGATCGAGAGCAGCAATCCGAGATTGGCTGGCTGCAG 1303

Qy  1201 GAGCTGCCGCGCGACTGAGACTCCTGGTGGCCGGCCAGCTGGAGGG 1250
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Db  1304 GAGCTGCTCGGGGCGCGACTCGGAGACCCCTACTGGTGGCCGGCCAGCTGGAGGG 1363

Qy  1251 AACAGCTCCGGCGACAACTGCAGCAGCAGCGGCGAGGGCCAACGGACGGGCTG 1320
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Db  1364 AACAGCTCCGGCGACAACTGCAGCAGCAGCGGCGAGGGCCAACGGACGGGGCTG 1423

Qy  1321 GAGCTGCTGGGGCGGCCCGTCGCGCGAGCGCCTACTCCCTACTCCGCACTC 1380
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Db  1424 GAGCTGCTAGGGCGGCCCGTCGCGCGAGCGCCTACTCCCTACTCCGCACTC 1483

Qy  1381 AGCAGGCCTCACCAGCGTGGGCTTCGGCGTCCGCAACACGGACACCGAGAGATC 1440
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Db  1484 AGCAGGCCTCACCAGCGTGGGGCTTCGGCGTCCGCAACACGGACACCGAGAGATCTCTCT 1543

Qy  1441 TTCTCCATCTGCACCATGCTCATCGGGCCGCATGCGCGGTGTGTTTGGGAACGTG 1500
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Db  1544 TTCTCCATGCCATCTGCACCATGCTCATCGGGCCGCATGCGCGGTGTGTTGTTCGGGAACGTG 1603
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Qy  1501 ACGGCCATCATCAGCGCCATGTGCACGCCGCCGCTTTCTGTACCACAAGCCGCACGCGGCAC 1560
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Db  1604 ACGGCCATCATCAGCGCCATCATCCGACGCGCCGCGCCGCTTTCTGTACCACAAGCCGCACGCGGCGAC 1663

Qy  1561 CTGCGCGGACTACATCCGCATCACCGTATCCCCTAAGCCCCTCCAAGCAGCGCCATGTGCGAG 1620
         |||||||||||||||||||||||| |||||||||||||||||||||||||| |||||
Db  1664 CTGCGCGGACTACATCCGCATCATCCGTACCCCTAAGCCCCTCAAGCAGCCATGCTGCGAG 1723

Qy  1621 TACTTCCAGGCCACCTGGGCGGTGAACAATGGCATGGCAGTCGACAACACCCAGCTGCTGCGAGAGC 1680
         ||||||||||||||| |||||||||  ||||| ||||||||||||||||||||||||||
Db  1724 TACTTCCAGGCCACCTGGGCGGTGAACAATGCATGGCAGTCGACAACACCCAGCTGCTGCGAGAGC 1783

Qy  1681 CTCCCTGACGAGCTGCGCGCGGCGCCAGCATCGCCACGTCCTCCACCGACTG 1740
         |||||||||||||||||||||||| |||||||||||||||||||||||||
Db  1784 CTCCCTGACGAGCTGCGCGCGGCGCCAGCATCGCCAGACACCGACTCGCACCGACTG 1843

Qy  1741 CCACTGTTGAGGCGGCACGCGCGGCCAGCGCGGCGCACTGTCTCTGCGGCCCTCGGGCCCC 1800
         ||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  1844 CCGCTGTTGAGGCAGCAGCGCGGCGGCCAGCGCGGCGCACTGTCTCTGCGGCCCTCGGGCCCC 1903

Qy  1801 GCCTTCTGCACGCGCCGGGGGGCGAGTACTCCATCATCCGCCCTGCCCTGCCCCATCCTAC 1860
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Db  1904 GCCTTCTGCACGCGCCGGGGGGCAGTACCTCATCATCCGCCCTGCCCTGCCCCATCCTAC 1963

Qy  1861 TTTGTCTGCTCTCTGGCTGGAGTGTGAGCTGCCCCCGCGGCGGCGGGGGCGGCGGCAGTC 1920
         |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1964 TTTGTCTGCTCTGGCTGGAGTGGAGCTGCCCCCGCGGCGGCGGGGGCGGCGGCAGTC 2023

Qy  1921 AAGGGGACCTGATCGGCTCGTGTGAGCTGCCCGGGGGCGGCAGGTGGTAAAGGCCAATGCC 1980
         ||||||||||| ||||| | ||||||| ||||||||||||||||||  ||||||||||
Db  2024 AAGGGGTGACCTGATCGGCTGTGTGAGCTGCCCGGGGGAGGGAGGTGGTAAAGGCCAAGCC 2083

Qy  1981 GACGTGAAGGGCTGACTACTGCGTCTCAGTGTGCTCAGTGCGCCTGGCCTGCACGAC 2040
         |||||| ||||||||||||| ||||||| |||| ||||||||||||||||||||
Db  2084 GATGTGAAGGGCTGACTACTGCGTCTCAGTTGCAGTGCGCTGGCCTGGCCTGCACGAC 2143

Qy  2041 AGCCTTCGCGCTGTACTTCGGGGCCCATCCTGGGCCGCTTCAGTCTCGGCCGGGAGCTC 2100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2144 AGCCTTCGCGCTGTTCCAGTGTTTCAGCCGTGGGCCGCTTCAGTCTGCCGGGAGGGGAGTC 2203

Qy  2101 AGCTACAACCTGGGTGTGGGGGAGGCTCTGCCAGTGTGGACTACAGCGCCTGGGC 2160
         ||||||||||||| ||||||||||||||||||| ||||||||||||||||||||
Db  2204 AGCTACAACCTGGGTGTGGGGGAGGCTCTGTCTGCAGAGTGGACCACAGCGCCTGGGC 2263

Qy  2161 GACAATACCCTTATGTCCACGCTGAGGAGAAGGAGCAGAGTGAAGGCTTGAAGGTTTTAC 2220
         ||||||||||| |||||||||||||||||||||||||||||||||| |||||||
Db  2264 GACAATACCCTTATGTCCACGCTGAGGAGGAGAAGGAGCAGAGTGAAGCTTTGAAGGCTTTTAC 2323

Qy  2221 GTCTCCCCAGCTGATGAGCCCCAGCCCTGATGAGCGCCCTGCTCCTGTCCCCTCGCACCTCC 2280
         ||||||||||||||||||||||||||||| ||||||||||||||||||||| |||||
Db  2324 GTCTCCCCAGCTGATGAGCCCCAGCCCTGATGAGCGCCCTGCTCACTGTCCCCTGGTTGCACCTCC 2383

Qy  2281 TCATCTCAGCTGCCAAGCTGCTCATCCCACGTGCCTATCCCGGCCTCGTCTAGGT 2340
         ||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db  2384 TCATCCTCGGCTGCCAAGCTGCTCATCCCACGTGCCTATCCCGGCCTCGTCTAGGT 2443

Qy  2341 GGCAGAGGGAGGCCCAGCGAGGGCTTTGAAGGCTGGAGGCGGTTTGAAGGCTGGAGGCGGTGCCCCACG 2400
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Db  2444 GGCAGAGGGAGAGCCAGCGAGGGCGTTTGAAGGCTGGAGGCGGTGCCCCCACA 2503

Qy  2401 CCACGGGCCTGTGAGGGGCTACGGCCATGTCCATGCGTTCCTCTACTTCCACCTG 2460
         |||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  2504 CCACGGGCCTGTGAGGGGCTACGGCCATGTCCATGCGTTCCTCTACTTCCACCTG 2563

Qy  2461 AGCAGCTCAGCTGCCAAGCTGCTGTGGCATTGAAGACGGCTGTAGAGACGCTGTGGCTCGACCAGGATC 2520
         ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  2564 AGCCCCAGGTAGTAGAGATGCATTGAAGACGCGTGGCTCGGCTGTAGAGACGCTGTGGCTCGACCAGGATC 2623

Qy  2521 TTCCGGCTGGGCGCACCATGCTGCGCCCTGGCCCCTGGGCTGGGCCCTGGACCAGAGAGC 2580
         |||||||||| ||||||||||||||||||||| |||||||||||||||||||||||
Db  2624 TTCCGGCATGGGCGCACCATGCTGCGCCCTGGCCCCCTGGCTGGGCCCTGGACCAGAGAGT 2683
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Query Match: 97.0%;   Score 3153;   DB 14;   Length: 3249;
Best Local Similarity   98.2%;   Pred. No. 0;
Matches 3189:   Conservative   0;   Mismatches   0;   Indels   60;   Gaps   0;

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Qy      1  ATGGCCGGCCATGCGGGGCTCCTGGCGCCTCAGAACACTTCCTGGACACCATCGCTACG  60
           |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db      1  ATCCGGCCATGCGGGGCTCCTGCGCCGCCAGAACACCTTCCTGGACACCATCGCTACG   60

Qy     61  CGCTTCGACGGCACGCACGCACAGTAACTTCGTGTGGCCAACGCCCAGGTCGGCGGGCTCTC  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  CGCTTCGACGGCACGCACGCACAGTAACTTCGTGTGGCCATAGGGAGGGTCCGTGCCTCGG  120

Qy    121  CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCCGGGCTGAGGTC  180

Qy    181  ATGCAGGGGGCTGTGCCTGCCTCCTTCCTTTATGGGCCAGACCAGTGAGCTCGTCCGC  240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  ATGCAGGGGGCTGTGCCTGCCTCCTTCCTTTATGGGCCAGACCAGTGAGCTCGTCCGC  240

Qy    241  CAACAGATCCGCAAGGCCCTGACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241  CAACAGATCCGCAAGGCCCTGACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC  300

Qy    301  CGGAAGAGGCGGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCATAAAGAATGAGAAA  360
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301  CGGAAGAGGCGGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCATAAAGAATGAGAAA  360

Qy    361  GGGGAGGTGGCTCTCTTCCTCTAGTCTCCACAAGGACATCAGCGAAACCAGAACCGAGG  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361  GGGGAGGTGGCTCTCTTCCTCTAGTCTCCACAAGGACATCAGCGAAACCAGAACCGAGG  420

Qy    421  GGCCCCGACAGATGAAGAGACAGTGGTGGCCGATATGGGCGGCACGATCC  480
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  GGCCCTGACAGATGAAGAGACAGTAGTGGCCGATATGGGCGGCACGATCC  480

Qy    481  AAAGGCTTCAATGCCAACCAAGGCAAGCACAAGGCACAAGGTCAAGGGGAGAAACCA  540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  AAAGGCTTCAATGCCAACCAAGGCAAGCACAAGGCACAAGGTCAAGGGGAGAAGGCAC  540

Qy    541  CTGCAGAAGCAGCCCAAGGGCAAGCACAAGTCAAAGGGGTGTTGGGAGAAACCA  600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  CTGCAGAAGCAGCCCAAGGGCAAGCACAAGTCAAAGGGGTGTTGGGAGAAGCCA  600

Qy    601  AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCCCCTTCACTGT  660
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  AACTTGCCTGAGTACAAAGTAGCGCCTCATCCGTTCATCCTGTTGCACTGT  660

Qy    661  GGGGCACTGAGAGCCACCTGGCATGGCTTCACCTGCTCGCCACACTCTATGTGGCTGTC  720
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  GGGGCGCTGAGGGGCCACCTGGCATGGCTTCATCCGCTCGCCAGCCGGGGCCCG  720

Qy    721  ACTGTGCCCTACAGCGTGTGTGAGCACAGCCAGTGCGCCGCCCGGGGCCCA  780
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Db    721  ACCGTGCCCTACAGCGTGTGTGAGCACAGCCAGTGCGCCGCCCGGGGCCCA  780

Qy    781  CCCAGCGTCTGACCTGGGCCTGGAGGTCCTTCATCGTGACATGTGCGAATTC  840
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Db    781  CCCAGCGTCTGACCTGGGCCTGGAGGTCCTTCATCCTCGACATTGTCGAATTC  840

Qy    841  CGTACCCATTCGTGTCCAAGTCGGGCACCAGTGGGTTGCCCAAAGTCCATTTGCCTC  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  CGTACCCATTCGTGTCCAAGTCGGGCACCAGTGGGTTGCCCAAAGTCCATTTGCCTC  900

Qy    901  CACTACGTCACCACCTGGTTCCTGGATGTCATCGGGCCGTGGCTA  960
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Db    901  CACTACGTCACCACCTGGTTCCTGGATGTCATCGGGCCCTTGACCTG  960

Qy    961  CATGCCTTCAAGGTCAAGTGTACTTCGGGCCCATCTGCTG  1020
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Db    961  CATGCCTTCAAGGTCAAGTGTACTTCGGGCCCACCTGCTG  1020
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Qy   2581  GGCTGCTCACTGTCCCCATGGGCCCAAGCGGAGGCAAGAACACACTGGACAAG  2640
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Db   2684  GGCCTGCTCACTGTCCCCATGGGCCCAAGCGAGGCAAGAACACAGACCACTGGACAAG  2743

Qy   2641  CTTCGGCAGGCGGTGACAGACTGTCAGAGCACAGGTGCTGCAGATGCGGAAGGACTGCAG  2700
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Db   2744  CTTCGGCAGGCGGTGATGAGCGTGACAACAGGTGCCTGCAGATGCGGAAGGACTACAG  2803

Qy   2701  TCACTTCGCAGCTGTGCAGCTTGTGTCTGGCGCCCCAGCGGAGGTCCGTGCCTGG  2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2804  TCACTTCGCGCAGCTGTGCAGCTTGTGTCTGGCGCCCCATAGGGAGGTCCGTGCCTCGG  2863

Qy   2761  GCATCGGGAGGGGCCGTGCCCAGCCACCTCCGGGCTTCTCTGCAGCCACTCG  2820
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Db   2864  GCCTCAGGAGGGGGCCCATGCCCAGCCACCACCTCCGGGCTTCTGCAGCCACTCG  2923

Qy   2821  GACACTGGGGGCATCCTCCTACTGCCTGCAGCCTCGCAGCCCTGCCTCGTCTTGTGAGTGGGGACT  2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2924  GACACTGGGGCATCCTCCTACTGCCTGCAGCCTGCTGCTGTTGTCTTGTGAGTGGGGACT  2983

Qy   2881  TGGCCCCACCCTGTCCGGGGCCTCCCCTCATGGCACCCTGGGCCTGGGGTCCCCA  2940
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Db   2984  TGGCCCCACCCTGTCCGGGGCCTCCCCTCATGGCACCCTGGGCCTGGGGTCCCCCA  3043

Qy   2941  GCGTCAGAGCTTCAGGACTTCTGGACCTCCACCTCAGAGCTCA  3000
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Db   3044  GCATCTCAGAGCTTCTGGACCTCCACCTCAGACTCA  3103

Qy   3001  GAGCCCCTGCCTCGAGGCCACACCCCTGCCTCCCCCTCCTCCACCTCAGACTCA  3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3104  GAGCCCCTGCCTCGAGGCCACACCCCTGCCTCCCCCTCCTCCACCTCTCCT  3163

Qy   3061  TCTGAGGAAGGGGCTAGGACTGGGCCCAGAGCCTGTGAGCGAGGCTGAGGCTACCAGC  3120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3164  TCTGAGGAAGGGGCTAGGACTGGGCCCCCAGAGCCTGTGAGCGAGGCTGAGGCTACCAGC  3223

Qy   3121  ACTGGAGAGCCCCCACCACAGGGTCAGGGGCCTGGCCTGGGACCCCCACAGCCTG  3180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3224  ACTGGAGAGCCCCCCGCCAGTGTCAGGGGCCTGGCCTGGGACCCCCACAGCCTG  3283

Qy   3181  GAGATGTGTGCTTATTGGGTTGCCATGGCTCTGGCACAGTCCAGTGTCTCTGGCACAGGACCA  3240
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3284  GAGATGTGTGCTTATTGGGTTGCCACGGCTCTGGCACAGTCCAGTGACCACGTGGACCCA  3343

Qy   3241  ACAGGGGTCTGA  3252
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Db   3344  ACAGGGGTCTGA  3355
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RESULT 6
US-10-185-867-3

RESULT 7
US-09-119-855-3
; Sequence 3, Application US/09119855
; Patent No. US20020099197A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: mni-055
; CURRENT APPLICATION NUMBER: US/09/119,855
; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 3240
; TYPE: DNA
; ORGANISM: Monkey
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3240)
US-09-119-855-3

Query Match   96.7%;   Score 3144; DB 9; Length 3240;
Best Local Similarity 98.1%;
Matches 3180;   Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy   10 ...
Db   1 ...

[DNA sequence alignment data]

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Db   1681 GAGCTGCGCGGCCAGACATGCCACCTGCACCTGCACAAGGAGGTCCTGCGAGCTGCCCGTGTTT 1740
Qy   2830 GCATCCTCCTACTGCCTGCCAGCCCCAGCTGGCTTGTCTTGAGTGGGACTTGGCCCAC 2889
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GCATCCTCCTACTGCCTGCCAGCCCCAGCTGGCTTGTCTTGAGTGGGACTTGGCCCAC 2880
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(DNA sequence alignment blocks — Query (Qy) and Database (Db) paired rows continue throughout the page)

RESULT 8
US-09-965-830-9
; Sequence 9, Application US/09965830
; Patent No. US20020177201A1
; GENERAL INFORMATION:
;   APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
;   TITLE OF INVENTION: A novel potassium channel protein
;   FILE REFERENCE: Y9903-PCT
;   CURRENT APPLICATION NUMBER: US/09/965,830
;   CURRENT FILING DATE: 2001-10-01
;   PRIOR APPLICATION NUMBER: 09/600,776
;   PRIOR APPLICATION NUMBER: JP 1998-346198
;   PRIOR FILING DATE: 2001-07-21
;   PRIOR FILING DATE: 1998-12-04
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 9
;   LENGTH: 3715
;   TYPE: DNA
;   ORGANISM: Rattus sp.
US-09-965-830-9

Query Match   81.9%; Score 2664.8; DB 10; Length 3715;
Best Local Similarity   89.0%; Pred. No. 0;
Matches 2905; Conservative 0; Mismatches 347; Indels 12; Gaps 2;

Qy   1 ATGGCCGGCCATGCGGGGCCTCCTGCGCCTCCTGGACCACCTTCCTGGACCATCGCTACG 60
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Db   156 ATGCCGGCCATGCGGGGCCTCCTGCGCCTCCTGGACCACCTTCCTGGACCATCGCCACC 215

Qy   61 CGCTTCGACGGACGGCCACGCAGTAACTTCGTCGTGCTGGCAGAGGG 120
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   216 CGCTTCGACGGACGGCCACGCAGTAACTTCGTCGTGCTGGCAGAGGG 275

Qy   121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGTTCTGC 180
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   276 CCTGTGGTCTACTGCTCTCCATGGCTTCTGTGACCTCACGGGTTCTGC 335

Qy   181 ATGCAGCGGGGTCGTGCTGCTGC?CCTTCCTTTATGGGCAGACACCAGTGAGTCGTCCGC 240
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   336 ATGCAGCGAGGTCGTGCTGCTGC?CCTTCCTTCCTCTATGGGCAGACCAGTGAGTGGTCCGC 395

Qy   241 CAACAGATCCGCAAGGCCCTGACGAGCACAAAGGAGTTCAAGCAGTTGATCCTGTAC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   ...
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Db          IIIIIIIIII II IIIIIIIIII IIIIIIII I IIIIIIII IIIIIIIIII IIIIIII      Db   1476  ACTGGCTGGAGCTGCTGGGGTGGCCCATCCTACGCAGCGCTACATCACCTCCTGTAC  1535
      395   CAACAGATCCGGAAAAGCCCTGGATGAGCACAAAGAATTCAAGGCTGAACTGATTCCTGTAC  455

Qy    301   CGGAAGAGCGGGCTCCCGTTCGGTGTCCTGGATGTGATACCCATAAAGAGAATGAGAAA  360   Qy   1372  TTCGCCACTCAGCAGCCTTCGGCACGGTCCGGGCTTCGGCAATGTCCGCTAACACAGGACACC  1431
Db    456   CGGAAGAGCGGGGCGGGGGCTTCCATTCTGTGTTCCTGGATGTGATACCCTATAAAAAACGAGAAG  515  Db   1536  TTCGCGCAGCAGTTCAGCACAGTGTGGCTTCGGCAATGTCCGCTAACACAGACACT  1595

Qy    361   GGGGAGGTGGCTCCTCCTTCCTAGCCTCTCACAAGGACATCAGCGAAACCAAGAACCGAGGG  420   Qy   1432  GAGAGAATCTTCTCCATCCGCACCATGTCATCCGTGATGCGTGTCTTCTGTACGGCGGTGGTGTTT  1491
Db    516   GGGGAGGTGGCCCTCTTCCTGTCTCTCACAAGGACTCAGTGAGACCAAGAACCGAGGA  575  Db   1596  GAGAGAATTTTCTCCATCGCACCATGTCTTATTGGAGTCTGATGCATGCAGTGGTGTTT  1655

Qy    421   GGCCCCGACAGATGGAAGAGAGACAGGTGGTGCCCGGCCGGCGCGATATGGCCGGCACGATCC  480   Qy   1492  GGGAACGTGACGGCCATCATCCAGCGCCATGTAGCCCGCGCTTCTGTACCACAGCGGC  1551
Db    576   GGCCCTGACAACTGGAAGAGAGAGAGGTGGTGCCCGACGCGATATGGTCGGGCAGGATCC  635  Db   1656  GGGAATGTGACGGCCATCATCCAGCGCCATGTAGCGCGCTCGCGCTTTCTGTACCACAGCCGC  1715

Qy    481   AAAGGCTTCAATGCCAACCGGCGGCGGGAGCCCGTGCTTCTTACCACCTGTCGTCCGGGCAC  540   Qy   1552  ACGGCGACCTGCGCGGACCTGCGCGGACTACACCACCGTATCCCCAAGGCCCCTCAAGCAGCGC  1611
Db    636   AAAGGCTTTAATGCCAATCGGAGGGCCGGACGGGGACCCGTTCTCTACCACCTCTCTGGTCAC  695  Db   1716  ACCCTGCCGACGCTGCGAGACGCACATTCGGCATCCACCGCACCCTCAAGCAGCGC  1775

Qy    541   CTGCAGAAGCAGCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGAGAAACCA  600   Qy   1612  ATGTGGAGTACTTCCAGGCCATCTGGGCGGTGAACAATGGCATCGACACCACCGAGCTG  1671
Db    696   CTGCAGAAACAACCCAAGGCAAGCACAAACTCAATAAGGGTGTGTTTGGAGAAGCCA  755  Db   1776  ATGCTCGAGTACTTCCAAGCCACCTGGGCCGTGAACAACGGCATCGATACCCACCTGAGCTG  1835

Qy    601   AACTTGCCTGAGTACAAAGTAGCCGCATCCGGAAGTCGCCCTTCATCCTGTTGCACCGT  660   Qy   1672  CTGCAGAGGCCTCCCTGACGAGCTGCGGCCAGCGACATCGCACCGTGCACCTGCGACAGGAGGTC  1731
Db    756   AATTTGCCCGAATATAAAGTCGCTGCTATCACCCTTTATCCTGCCTGCACTGT  815  Db   1836  CTGCAGAGCCTTCCGGATGAGCTTCGAGCAGCAGCATCGGCACCTGCACAAGGAGGTC  1895

Qy    661   GGGGCACTGAGAGCCACCTGGATGGCTTCATCCGCTCGCACACTCTATGTGGCTGTC  720   Qy   1732  CTGCAGCTGCCACTGTTTGAGGCGGCCAGCCGCCGGCCGTGCTGGCGCACTGTCTCTGGCC  1791
Db    816   GGGGCTCTGAGAGCCACCTGGATGGCTTCATCCGCTCGCACACTCTACGTGGCTGTC  875  Db   1896  CTGCAGCTGCCCATTGTTCGAGGCAGCAGCCGGCCGTGCTGGCGCACTGTCTCTGGCC  1955

Qy    721   ACTGTGCCCTAGACGCGTGTGTGATGCACAGCAGCGTGGTGTGATGCCGCGCCCCCCAGTGCGGCGCCCCCCG  780   Qy   1792  CTGCGGCCCGCCTTCTGCACGCGCGGGAGTACCTCATCCACCAAGGCGATGCCCTGCAG  1851
Db    876   ACTGTGCCATACAGCGTGTGTGTGAGCACAGCACCACGGAGCACCGGAGCCCAGTGCTGCCCCTGGGCCCA  935  Db   1956  CTGAGGCCCCGCCTTCTGCACGCGCGGGGAGTACCTCATTCACCAAGGCGATGCTCTCCAG  2015

Qy    781   CCCCTACTTGTCGTGACCTGGCCGTGGAGGTCCTTCTCATCCTTGACATTGTGCTGAATTTC  840   Qy   1852  GCCCCTACTTGTCGTCCTGGCTCTCAAGGTGCTCAAGGTGGCCACCGTGTCGGCC  1911
Db    936   CCTAGTGTCTTGTGACCTGGCCGTGGAGTCCTTCTCATCCTTCATCTTTGACATTGTGTGCTGAATTTT  995  Db   2016  GCTCTCTACTTTGTGTCTGCTCAAGGTTCCATGGAGGTCGCACCGTGCCCCGCC  2075

Qy    841   CGTACCACATTCGTGTCCAGTGGTGTTGGCCCAAGTGCCATTTGCCTC  900   Qy   1912  ATCCTAGGGAAGGGCGACCTGATCGGCGGCGTGCTGTGAGCGGGAGGCAGGTGGTAAAG  1971
Db    996   CGTACTACATTTGTGTCCAGTCAGGCCAGTGGTATTGCCCCCAAAGTCCATTTGCCTC  1055  Db   2076  ATTCTAGGGAAGGGTGACCTGGTCGGCGGCGTGCTGTGAGCAGCAGCAAGTAGTGAAG  2135

Qy    901   CACTACGTCACCACCTGGTTCCTGCTGGAGGTCCATCGGCAGCGGAATCCGGCAGCA  960   Qy   1972  GCCAATGCCGACGTGAAAGGGCTGACGTACGTCGCGTCCAGCTGGCTGGCTGGCC  2031
Db    1056  CACTACGTCACCACCTGGTTCCTGCTGCTGGAGGTCAGGGCTGAGGGTCAGGGTCAGCGGAGCACTGCCTACCTA  1115  Db   2136  GCCAATGCCGACGTGAAAGGGCTGACATACTGCGTCCTACAGTGCCTGCTGGG  2195

Qy    961   CATGGCCTTCAAGGTCAACCGTATCTCGGGGCCCATCTGCTGAAGACGTGGCCGCTGCCG  1020  Qy   2032  CTGCACGACAGCCTTGCGCTGCTACCCCGAGTTGCCCCGCGCTTCAGTGCGGTCCGA  2091
Db    1116  CATGGCCTTCAAGGTCAACGTGTGTGTACTGGTACCGTGGGGCTCCGTGCGCGGCTGCCTT  1175  Db   2196  CTGCACGAGAGCCTGCCACTGTACCCGAGTTTGCCCCGCGCTTAGGCAGGAGGTGGCCCTGGGCCTCCGA  2255

Qy    1021  CGCCTGCTGCCCCTACTACCAAGACTGACCGGCCGGTTCCTGTTGTGTCCC  1080  Qy   2092  GGGGAGCTCAGCTGCTACAACCTGGTGCTGAGGTGCTGGCTCTGCAGAGGAGGTGGACCAGCTCC  2151
Db    1176  CGGCTGCTGCCCCTACTACCAAGACTGACCGGCCGGTTCCTCTCTCAGTAGCCGGCTGCCTT  1235  Db   2256  GGGGAGCTCAGCTAGCAACCTGGAGCTGGAGGTGCTGCAGAGGTGGATAACCAGCTCA  2315

Qy    1081  ACACTGCTCATGGCCGTGTTCCGGCCTCGCGTTCGCCCTTCGGCCTTGCGTC  1140  Qy   2152  CTGAGCGGCGACAATACCCTTATGTCCACGCTGGAGGAGGAGGACAGATGGGGAGCAG  2211
Db    1236  ACCTTGCTCATGCGCTGTGTTTGCCCGCCGCCGCTGGGTGGCCTGGTTTGGTTCTTAC  1295  Db   2316  CTGAGTGGTGACAACACCCTCATGTCCACTGGAGGAGGAAGGAGACAGTGGGGAGCAA  2375

Qy    1141  ATTGGCCAGCAGGGGGAGAGATCGAGAGGCCAGGCGAATCGCAGCAGGAGATTGGGCTGCAG  1200  Qy   2212  GGCCCCACCGGTCTCCCCAGCCGCTGATGAGCCCCTGCGTCTGCCCCTGGC  2271
Db    1296  ATCGGCCAGCAGGCGCACGGCAGGGCGAGTCCAGATGGAGCGGCTGGCTGGCTGCTGCAG  1355  Db   2376  GGACACCGGACGATCTCACCAGCCCCAGCAGCCCCTGCGTCTCGTCACCTGGC  2435

Qy    1201  GAGCTGCCGCCCCGGCGCCCGACTGCGGCCTCCTACACCCGTGTGGCGGAGGGCCAGCTGGAGGG  1260  Qy   2272  TGCACCTCCTCATCCTCAGCTGCCATCCCCAACGTGCTATCCCCACCGCCCCGGCCT  2331
Db    1356  GAGCTGCCGCAGGCTGGCACGCAGCCTGGAGACCCCGTTATTACCTGGTGACCGCCAATGGGAGGG  1415  Db   2436  TGTACCTCCCTCCTCCAGCTGCCAAACTACTCTCCCCACGTGCACCCCGGCCG  2495

Qy    1261  AACAAGCTCCGGCAGTGACAACTGCAGCAGCA------GCAGGGCCAACCGGG  1321  Qy   2332  CGTCTAGGTGCAGAGGGCGGCCAGCAGGAGGCTTTGAAGGCTGGCGCC  2391
Db    1416  AACAAGCTCTGGCCAGCAAGAAAAACTGCAGTAGCAGTGGCGGCGGCGAAGCCCAACCGGG  1475  Db   2496  AGGCTGGGGTTGCCAGAGGCGGGCCCAAGTAGGGCAGGAGGGTTTTGAAGGCTGCGTGGTTGTCCT  2555

Qy    1312  ACGGGGTGGAGCTGCTGGGCGCCGCTGCGGCCGCGCTGCGCAGGCCTGCGCAGGCCTGCGCGCTCTGGCCTCCCTCTAC  1371  Qy   2392  TCTGCTCCATCCAGCGGACACTTGATGGGTTTGCAGCTGCGCCCCCATGCCCATGGAATGTGCCCC  2451
Db                                                                       Db   2556  TCTGCTCATCCATCCACCGGACAACCTGATGGGTTGCGAGCTGCGCCCCCATGCCCCATGGAATGTACCT  2615
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 3064
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(3057)
US-09-965-830-5

Query Match             27.2%;  Score 884.8;  DB 10;  Length 3064;
Best Local Similarity   65.5%;  Pred. No. 4.1e-210;
Matches 1408;  Conservative 0;  Mismatches 622;  Indels 120;  Gaps  3;

Qy         1 ATGCCGGCCATGCGGGGCCTCCTCGCGCCTCCTGGACACCTTCCTGGACAACACTTCCTGGACCATCGCTACG 60
             ||||||| |||  || |  || |||||  ||| |||||||||||||||||||||||| |||  ||
Db         4 ATGCCGGTCATGAAGGGGTTGCTGGCCCGCAAAACACCTTCCTGGACACCATCGCCACC 63

Qy        61 CGCTTCGACGGCACGCACGTAACTTCGTGCTGCGGCAACCGCCAGGTGGCGGGGGGCTCTTC 120
             ||||| |||| || |   || |  | ||| |  ||| ||||  | ||| || ||  ||
Db        64 CGTTTTACGGAACGCACGCACAACTTCCTGCTGGCGGCAACTTCCTGCTGCGGGGCCACAGGGGCTTT 123

Qy       121 CCCGTGCTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCGCTTCTCCCGGGCTGGAGGTC 180
             ||||| |  ||||| |  | |||  | ||| ||  ||  || | ||   ||||  |||||||
Db       124 CCCATCGTCTACTGCTCCGACGGCTCACAGGCTCGCGAGCTCACAGGCTCGCACCGAGGTC 183

Qy       181 ATGCAGCGGGGCTGTGCCTCCTCCTTTATGGCCAGACACCAGTGAGCTCGTCCGC 240
             |||  ||||| ||||  | | |  ||   |||  |  |||  |   |||  | |
Db       184 ATGCAGAGACCTGCAGCTGCCGTTCCTCTACGGCCACCAGGACCAGAGCCAGCCTG 243

Qy       241 CAACAGATCCGGCAAGGCCTGACGACGACCAAGAGTTCAAGGTCGAGCTGATCCTGTAC 300
             ||   |   |||  |  |||| ||| | |||  |  ||| ||| || ||||  |  ||||
Db       244 CAGGGTCTGCACAAACCCTGCAGGGAGCACCCGAGGCACCCGGGCTGAAATGTCGTTCTAC 303

Qy       301 CGGAAAGAGGGCTCCCGTTCTGCTGTCTCCTGATTGTGATACCCATAAAGAATGAGAAA 360
             |||  | |||  || ||  | |   |   |  |  ||  ||| ||  |  |||  ||
Db       304 CGCAAGGATGGCTCAGCCTTTGGCCTCCTGGACATGAATCAAGAATGAGATG 363

Qy       361 GGGGGAGGTGGCTCTCTTCCTAGTCTCTGCACAAGGACCATC-----AGCGAAACCAAGAAC 414
             ||||| ||||| || ||  |  | | | |  |  |||| |||      ||||  |||  |||
Db       364 GGGGAGTCGTGCTGTCTGTTCCTCTTTTCCTCAAGGATATCACTCAGGATAATCACTCAGAGTGGAAGCCCAGGA 423

Qy       415 CGAGGGGCCCCACAGATGATGGAAGGAGAGAACAGAGTGGTTGCCGGGCCA 474
             |||||||  ||| ||  | | ||| ||| |  |  |  ||||||||||
Db       424 CTTGGCCCCCTCCTGAGGAGGAGGCTAGGACTGGGACTGGAAAACTCCCTTGGTAGAAGGGGA 483

Qy       475 CGATCCAAAGGCTTCAATGCCAACCGGGGGGGACGGAGGCCGTGCTCTACCACCTGTCC 534
             |||||| ||| ||      |||  |||| || |  ||| |  | |  | |  || | ||
Db       484 GCCACCTGGAAATTTCGGTCTGCCGGCACCTTGGAGTGCTGTGTCTCACCCACTGACC 543

Qy       535 GGGCACCTGCAGAAGCAGCCCAAGGCCAAGCACAGTCAATAAGGGGTGTTGGGGAG 594
             |||||  ||| || ||  | |||||||  ||  | |   ||| | |||  |||||
Db       544 GGCCACTTTGGCCGCGGGGGCCAGGGAGGCCAATAATAAACGTGTTTGAGCCA 603

Qy       595 AAACCAAACTTGCCTGAGTACAAAGTAGCCCATCCGAAGTCGCCCTTCATCCTGTTG 654
             |||  || |  || |  ||| |  | |  | |  |  |||  |  ||||    |  |
Db       604 AAGCCATCAGTGCCCAGGGTACAACGGTCCCTCCTCGCCCTGTGGGGGGTCTCCGCTCCTCCTC 663

Qy       655 CACTGTGGGGCACTGAGAGCCTATGTG 714
             ||||  | |  |    |||||  | |||
Db       664 CACTACAGCGTCCAAGCCACTCGGACGGCCTTATCCTCCTTGCCACCTTCTACGTT 723

Qy       715 GCTGTCACTGTGCCCTACGCGTGTGTGAGCACGACAGCAGCACGGGTCTCCATCATTGTGCTG 774
             || || |  ||||   ||    | |||    |  ||| ||| | |  | |  || |  | |
Db       724 GCGGTCACCGTCCCTACCACAATGTCTGTTTCGGGTGACGATGACACCCCCATCACTTCG 783

Qy       775 GGCCCGCCAGCGTCTGTGACCTGGTCTTCATCCTGTGACATTGTGCTG 834
             ||||| |||||| | |||| ||| || | |  |    |||||| |||
Db       784 CGACACACCCTGTCAGGCGACATCGCGTGGAAATGCTCTTCATCCTAGATATCATCCTG 843

Qy       835 AATTCCGTACCACATTCGTGTCCAAGTCGGTGGTTGGCCCAAAGTCCATT 894
             ||||| || |  ||  | | ||||| ||| ||| | |||  ||||  ||||
Db       844 AACTTCCGCACCACTATGTGTCCCAGTCCGGCCAGTAATCTCTCGTCCTCGTTCCATT 903
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Qy      2452 CCAGATCTGAGCCGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACCAGCCC 2511
             |||| ||||||||||  |  |   |||| |||||  || |||||||||||| |||||||
Db      2616 CCAGACCTGAGCCGGTCGTAGATGGCATTGAAGACGGCTGCGGCTCTGACCAGCAC 2675

Qy      2512 AAGTTCTCTTTCCGGCGTGGCCAGTCTGGCCCGGAATGTAGACAGCAGCCCCTCCCCTGGA 2571
             ||||||||||| |||| | ||| |||  | |||||  | ||||||||||||| || |
Db      2676 AAGTTCTCTTTCCGGGTGGGTCAGTCTGGCCCCAGAATGTAGACAGCAGCCCCTCCCCAGGA 2735

Qy      2572 CCAGAGAGGCGGCCTGCTCACTGTTCCCCATGGGCCAGCAGGCAAGGAGCAAGAACACAGACACA 2631
             ||||||| ||||  |||||||| |||||||||||||||||||| |||  ||  ||||||| |||
Db      2736 ACAGAGAGTGGCCTGCTCACTGTCCCCAGTGCCCAGTGCCCAGTGCCCAGGTAGAGGCAAGAAAACACAGACACA 2795

Qy      2632 CTGGACAACGCTTCGGCAGCGGCCGGTGACGAGCTGTCAGACGAGCTGGCTGCCGCAGATCGCGGGAA 2691
             |||||| ||||  || || | ||||||| || || | ||||   ||| | | ||  ||| ||| |||
Db      2796 CTGGACAAGCTACGGCAGCCCAGGCGGTGACGAGCTGTCTGAACAGTGCTCAGACATGCGAGAG 2855

Qy      2692 GGACTGCAGTCACTTCGGTGCCTGCCAGCTGTGCAGCTTGTCCTGCGCGCCCACAGGAGGGTCCG 2751
             ||| || ||| | |||| | |||| || ||||| ||||| | |  |  |  | |  || |||
Db      2856 GGACTGCAGTCACTTCGCCAGCCTGTGCAGCTCATCCTGGTGCCCCAAGGGAAGGCCACAGGGGCTTT 2915

Qy      2752 TGCCCTCGGGCATGGGAGAGGGCGTGCCCAGCAGCACCTCCGGGCTTCTGCAGCC 2811
             || ||  ||| || | ||| | |   ||  |||| |  | |   || | | ||||
Db      2916 TGTCCCGGGTATCAGGAGGGCCCATGCCCAGCCTCTCTACAACCC 2975

Qy      2812 CTGTGTGTGGACACTGGGGCATCCCTCTACTGCTGGGGCTGGCTGGTGTCCGC 2871
             ||||| || |||||| | |  ||| |  | |||| ||| || ||    |  |
Db      2976 CTGCGTGTGACACTGGGGCATCATCCTACTGCTGGGGCTCAGCAGGTTCAGTCTTG 3035

Qy      2872 AGTGGGACTTGGCCCCCACCCCGTCCGGGGCCT--CCTCCCCCTCATGGCCACCTGGCCC 2928
             |||||||||||| ||| | || ||  |  |     | |  |||||  | ||| | ||| ||
Db      3036 AGTGGGACTGGCCTCACCCCGTCACCCCCGTCCAGGGATCCCCGTCCCCTCATGGCCACCTGGCCC 3035

Qy      2929 TGGGGTCCCCCAGCGTCTCAGAGCTCCCCCTGGCCTTGCCTTGCTGAGCTT-CTGGACCTCC 2988
             ||||| ||||| ||| |||||||| ||   | |||| |  ||  |||||||  |||||||||
Db      3096 TGGGGCCCCCCAGCATCTCAGAGCTCCCCCTGGGCCTGCCGGCCAGCTTTATGGACCTCC 3155

Qy      2989 ACCTCAGACTCAGAGCCCCCTGCCTGCTCTGAGCCCCAGCACCCCTGCC 3048
             ||||||||||||||||||||| | |||||||||||| || |||||||||
Db      3156 ACCTCAGACTCAGAGCCCCCTGGCTGCTCTGAGCCCCAGCCAGCACCACCCCAGCC 3215

Qy      3049 TCCCTCCTTCCTTCTGAGGAAGGGGCTAGGAGCTGGGCCCGCAGAGCTGAGCGGGCT 3108
             || | |||| |||||||||| ||| | ||||| | || || ||||| |  |||||
Db      3216 TCACCCCCTCCTCCTGAGGAAGGAGGCTAGGACTGGGACTCGTGAGCCAGGCT 3275

Qy      3109 GAGGCTACCAGCACTGAGAGCGCCCCCACCAGGGTCAGGGGCCTTGGGCCTTGCCCTGGGAC 3168
             ||||||||||| |||||||| ||||||  | |  | || || || || ||||  || |||
Db      3276 GAGGCTACCAGTACTGAGAGCGCCCCCATCTGGGGTCAGGGGGCCTTCAGGGGCCTTGCCCCTGGAT 3335

Qy      3169 CCCACAGCCTGGGAGATGGTGCTTATTGGCTGCCATGGGCTCTGCGCACAGTCCAGTGGACC 3228
             |||||||||||| |||||| ||| ||||||| | |||| ||| | |||  |  |||||||  |
Db      3336 CCCACAGCCTGAGAGTGGTGCTGATGTCTCATCGGCATCGGCTGCCCATGCCGGTCTCGGTCCCAGTGGACC 3395

Qy      3229 CAGGAAGAAGGCACAGGGGTCTGA 3252
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Db      3396 CAGGAGGAGGGCACAGGAGAGTCTGA 3419
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RESULT 9
US-09-965-830-5
; Sequence 5, Application US/09965830
; Patent No. US20020177201A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/965,830
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 09/600,776
; PRIOR FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: JP P1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
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RESULT 10
US-09-965-830-10
; Sequence 10, Application US/09965830
; Patent No. US2002017201A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: A novel potassium channel protein
; FILE REFERENCE: Y9903-PCT
; CURRENT APPLICATION NUMBER: US/09/965,830
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 09/600,776
; PRIOR FILING DATE: 2001-07-21
; PRIOR APPLICATION NUMBER: JP 1998-346198
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 3736
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-965-830-10

Query Match   26.78%; Score 869.8; DB 10; Length 3736;
Best Local Similarity 65.38%; Pred. No. 2.3e-206;
Matches 1403; Conservative 0; Mismatches 627; Indels 117; Gaps 4;

RESULT 11

US-09-119-855-9

: Sequence 9, Application US/09119855

: Patent No. US20020099197A1

: GENERAL INFORMATION:

:   APPLICANT: Curtis, Rory A.J.

:   TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

:   FILE REFERENCE: mni-055

:   CURRENT APPLICATION NUMBER: US/09/119,855

:   CURRENT FILING DATE: 1998-07-21

:   NUMBER OF SEQ ID NOS: 13

:   SOFTWARE: PatentIn Ver. 2.0

: SEQ ID NO 9

:   LENGTH: 870

:   TYPE: DNA

:   ORGANISM: Homo sapiens

:   FEATURE:

:   NAME/KEY: CDS

:   LOCATION: (1)..(870)

US-09-119-855-9

  Query Match   26.0%; Score 844.4; DB 9; Length 870;
  Best Local Similarity   99.9%; Pred. No. 3.8e-200;
  Matches 845; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 ATGGCGGCCATGCGGGCCTTCCTGGCGCCTCAGAAACACTTCCTGGACACCATCGCTACG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGCGGCCATGCGGGCCTTCCTGGCGCCTCAGAAACACTTCCTGGACACCATCGCTACG   60

Qy   61 CGCTTCGACGGCACGCACGGTAACTTCGTGTCGTGGCAACGCCACAGTAACTTCGTGTCTTC   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CGCTTCGACGGCACGCACGGTAACTTCGTGTCGTGGCAACGCCACAGTAACTTCGTGTCTTC   120

Qy   121 CCCGGTCGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGCGTTCTTCCGGCTGAGGTC   180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

; LOCATION: (1)..(870)
US-10-185-867-9

Query Match   26.0%;   Score 844.4; DB 14; Length 870;
Best Local Similarity 99.9%;   Pred. No. 3.8e-200;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 ATGGCCGGCCATGCGGGGCCTCGGGGCCTCAGAACACTTCCTGGACACATCGGCTACG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGCCGGCCATGCGGGGCCTCGGGGCCTCAGAACACTTCCTGGACACATCGGCTACG 60

Qy     61 CGGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGCCCAGTGGCCGGGCTCTTC 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CGGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGCCCAGTGGCCGGGCTCTTC 120

Qy    121 CCGTGGTCTACTGCTCTGATGGCTCTGTGACCTCACGGGCTCTCCCGGGCTGAGGTC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGTGGTCTACTGCTCTGATGGCTCTGTGACCTCACGGGCTCTCCCGGGCTGAGGTC 180

Qy    181 ATGCAGCGGGGCTGTGCCCGGCCTCCTTATGGGCCAGACTGAGCTGAGCTCGTCCGC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ATGCAGCGGGGCTGTGCCCGGCCTCCTTATGGGCCAGACTGAGCTGAGCTCGTCCGC 240

Qy    241 CAACAGATCCGCAAGGCCCTGGACGAGCACGCACAAGGACAGTTCAAGGCTGAGCTGTAC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAACAGATCCGCAAGGCCCTGGACGAGCACGCACAAGGACAGTTCAAGGCTGAGCTGTAC 300

Qy    301 CGGAAGAGCGGCGTCCCGTTCTGGTGTCTCCTGCGATGTGATACCCATAAAGAATGAGAAA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGAAGAGCGGCGTCCCGTTCTGGTGTCTCCTGCGATGTGATACCCATAAAGAATGAGAAA 360

Qy    361 GGGGAGGTGGCTGTCTCTTCCTCCAGTCTCCGGCCGGGCGACAGGTGGCCGGGCACGAGGG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGGGAGGTGGCTGTCTCTTCCTCCAGTCTCCGGCCGGGCGACAGGTGGCCGGGCACGAGGG 420

Qy    421 GGCCCCGACAGATGGAAGGAGAGCCGGGGCGGCCGGGCGCGATATGGCCGGCACGATCC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCCCCGACAGATGGAAGGAGAGCCGGGGCGGCCGGGCGCGATATGGCCGGCACGATCC 480

Qy    481 AAAGGCTTCAATGCCAACCGCGCCCGTGCTCTACCACCTGCCCGGGCAC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAAGGCTTCAATGCCAACCGCGCCCGTGCTCTACCACCTGCCCGGGCAC 540

Qy    541 CTGCAGAAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CTGCAGAAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTTGGGGAGAAACCA 600

Qy    601 AACTTGCCTGAGTACAAAGTAGGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACTTGCCTGAGTACAAAGTAGGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT 660

Qy    661 GGGCACTGAGAGCCTACAGCGTGTGTGAGCAGCAGCACGGGGGCGGCCG 720
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Db    661 GGGCACTGAGAGCCTACAGCGTGTGTGAGCAGCAGCACGGGGGCGGCCG 720

Qy    721 ACTGTGCCCTACAGCGTGTGTGAGCAGCAGCACGGGGGCGGCCG 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 ACTGTGCCCTACAGCGTGTGTGAGCAGCAGCACGGGGGCGGCCG 780

Qy    781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCCTCTTCATCCTTGACATTGCTGAATTTC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CCCAGCGTCTGTGACCTGGCCGTGGAGGTCCTCTTCATCCTTGACATTGCTGAATTC 840

Qy    841 CGTACC 846
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Db    841 CGTACC 846
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RESULT 13
US-09-119-855-7
; Sequence 7, Application US/09119855
; Patent No. US20020099197A1
; GENERAL INFORMATION:

RESULT 12
US-10-185-867-9
; Sequence 9, Application US/C0185867
; Publication No. US2003010442A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/10/185,867
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/358,383
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: mni-055
; CURRENT APPLICATION NUMBER: US/09/119,855
; CURRENT FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (263)..(1132)
US-09-119-855-7

Query Match   26.0%; Score 844.4; DB 9; Length 1132;
Best Local Similarity 99.9%; Pred. No. 4e-200;
Matches 845; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy   1 ATGGCCGGCCATGCGGGGGCCTCCTGGCGGCCTCAGAACACCTTCCTGGACACCATCGCTACG 60
          |||||||||||||||||||||||||||| |||| ||||||||||||||||||||||||||||
Db   263 ATGGCCGGCCATGCGGGGGCCTCCTGGCCGCCCGAGAACACCTTCCTGGACACCATCGCTACG 322

Qy   61 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGGGCCAGGTGGCGGGGCTCTTC 120
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   323 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGTGGGCCAGGTGGCGGGGCTCTTC 384

Qy   121 CCGGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTCTCCCGGGCTGAGGTC 180
          |||||||||||||||| ||||||||||||||||||||||||| ||||||||||||||||
Db   383 CCGGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTCTCCCGGGCTGAGGTC 442

Qy   181 ATGCAGCGGGGGCTGTGCCCTTTATGGGCCAGCAGCACCAGCAGCTGTCCGC 240
          ||||||||||||||| |||||||||||||||| |||||||||||||||||||
Db   443 ATGCAGCGGGGGCTGTGCCTGCCCTTTATGGGCCAGCAGCACCAGCAGCTGTCCGC 502

Qy   241 CAACAGATCCGCAAGGCCCTGGACAGCAGCAAGGAGTTCAAGGCTGAGCTGTAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   503 CAACAGATCCGCAAGGCCCTGGACAGCAGCAAGGAGTTCAAGGCTGAGCTGTAC 562

Qy   301 CGGAAGAGCGGGCTCCCGTTCTGTGTCTCCGATGTGATACCCATAAAGAATGAGAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   563 CGGAAGAGCGGGCTCCCGTTCTGTGTCTCCGATGTGATACCCATAAAGAATGAGAAA 622

Qy   361 GGGGAGGTGGCTGCTCTTCCAGTCTCTCACAAGGAGCAATCAGCGAAACCAAGAACCGAGGG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   623 GGGGAGGTGGCTGCTCTTCCAGTCTCTCACAAGGAGCAATCAGCGAAACCAAGAACCGAGGG 682

Qy   421 GGGCCCGACAGATGGAAGGAGAGACAGTGTGGCGGCCGGCCGATATGGGCGGGCACGATCC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   683 GGGCCCGACAGATGGAAGGAGAGACAGTGTGGCGGCCGGCCGATATGGGCGGGCACGATCC 742

Qy   481 AAAGGCTTCAATGCCAAGGCCCAAGGTCAATAAGGGGTGTTTGGGGAGAAACCA 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   743 AAAGGCTTCAATGCCAAGGCCCAAGGTCAATAAGGGGTGTTTGGGGAGAAACCA 802

Qy   541 CTGCAGAAGCAGCCAAGGGCAAGCAAGCTCAATAAGGGGCTCAATAAGGGGCTCATTGGCTGCACTGT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   803 CTGCAGAAGCAGCCAAGGGCAAGCAAGCTCAATAAGGGGGTGTTTGGGGAGAAACCA 862

Qy   601 AACTTGCCTGAGTACAAAGTAGCCGCCAAAGTCGCCCTTCATCCTGCTCCCCACACTCTAGTGTGCTGT 660
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Db   863 AACTTGCCTGAGTACAAAGTAGCCGCCAAAGTCGCCCTTCATCCTGTTGCCACTGT 922

Qy   661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCCGCCCACACTCTATGTGCGTCGTGT 720
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Db   923 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACTCTATGTGGCTGTC 982

Qy   721 ACTGTGCCCTACAGCGTGTGTGAGCACAGCAGCACGGAGCCCGGGCCCCG 780
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   983 ACTGTGCCCTACAGCGTGTGTGAGCACAGCAGCACGGAGCCCGGGCCCCG 1042

Qy   781 CCCAGCGTCTGTGACCTGGCCGTGGAGTCCTCTTCATCCTTGACATTGTGCTGAATTC 840

; RESULT 14
; US-10-185-867-7
; Sequence 7, Application US/10/185867
; Publication No. US20030104429A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-055CP
; CURRENT APPLICATION NUMBER: US/10/185,867
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/358,383
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: USSN 09/119,855
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (263)..(1132)
US-10-185-867-7

Query Match   26.0%; Score 844.4; DB 14; Length 1132;
Best Local Similarity 99.9%; Pred. No. 4e-200;
Matches 845; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 ATGGCCGGCCATGCGGGGGCCTCCTGGCGGCCTCAGAACACCTTCCTGGACACCATCGCTACG 60
          |||||||||||||||||||||||||||| |||| ||||||||||||||||||||||||||||
Db   263 ATGGCCGGCCATGCGGGGGCCTCCTGGCCGCCCCAGAACACCTTCCTGGACACCATCGCTACG 322

Qy   61 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGCCCAGGTGGCGGGGCTCTTC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   323 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACGCCCAGGTGGCGGGGCTCTTC 382

Qy   121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   383 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGCTTCTCCGGGCTGAGGTC 442

Qy   181 ATGCAGCGGGGGCTGTGCCTGCCCTTTATGGGCCAGCAGCACAAGGCACAAGCAAGTTCAAGGCTGAGCTGTAC 240
          |||||||||||||||||||||||||||||||||||||||||
Db   443 ATGCAGCGGGGGCTGTGCCTGCCCTTTATGGGCCAGCAGCACAAGGCACAAGCAAGTTCAAGGCTGAGCTGTAC 502

Qy   241 CAACAGATCCGCAAGGCCCTGGACAGCAGCAAGGAGTTCAAGGCTGAGCTGTAC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   503 CAACAGATCCGCAAGGCCCTGGACAGCAGCAAGGAGTTCAAGGCTGAGCTGTAC 562

Qy   301 CGGAAGAGCGGGCTCCCGTTCTGTGTCTCCGATGTGATACCCATAAAGAATGAGAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   563 CGGAAGAGCGGGCTCCCGTTCTGTGTCTCCGATGTGATACCCATAAAGAATGAGAAA 622

Qy   361 GGGGAGGTGGCCGTTCTCTGTCTCCAGTCTCTGACCTCACGGGCTTCTCCGGGCTGAGGTC 420
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Db   623 GGGGAGGTGGCCGTTCTCTGTCTCCAGTCTCTCACAAGGACCAAGAACCAAGAACCGAGGG 682

Qy   421 GGGCCCCGACAGATGGAAGGAGAGACAGTGTGGCGGCCGGCCGATATGGGCGGGCACGATCC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   683 GGGCCCCGACAGATGGAAGGAGAGACAGTGTGGCGGCCGGCCGATATGGGCGGGCACGATCC 742

Qy   481 AAAGGCTTCAATGCCAACCGTCTCTACCACCTGTCCGGGCAC 540
          ||||||||||||||||||||||||||||||||||||||||||
Db   743 AAAGGCTTCAATGCCAACCGTCTCTACCACCTGTCCGGGCAC 802

Qy   541 CTGCAGAAGCAGCCCAAGGGCTCATTTGGGGCAGCTCAAGGCACAAGGCACAAGGAGTTCAAGGCTGAGCTGTAC 600
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   803 CTGCAGAAGCAGCCCAAGGGCTCATTTGGGGCAGTTCAAGGCACAAGGCACAAGGAGTTCAAGGCTGAGCTGTAC 862

Qy   601 AACTTGCCTGAGTACAAAGTCGCCGCCTCTTCATCCTGCTCCGCCCACTCTATGTGCTGT 660
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Db   863 AACTTGCCTGAGTACAAAGTCGCCGCCTCTTCATCCTGCTCCGCCCACTCTATGTGCTGT 922

Qy   661 GGGCCACTGAGAGCCCCCGATATGGCCGCCCGATATGGCCGCCCGATATGCCCGGACGATCC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   923 GGGCCACTGAGAGCCCCCGATATGGCCGCCCGATATGGCCGCCCGATATGCCCGGACGATCC 982

Qy   721 ACTGTGCCCTACAGCGTGACCGTGGAGCACAGCAGGTTCTACCACCTGTCCGGGCAC 780
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Db   983 ACTGTGCCCTACAGCGTGACCGTGGAGCACAGCAGGTTCTACCACCTGTCCGGGCAC 1042

Qy   781 CCCAGCGTCTGTGACCTGGCCGTGGAGTCCTCTTCATCCTTGACATTGTGCTGAATTC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1043 CCCAGCGTCTGTGACCTGGCCGTGGAGTCCTCTTCATCCTTGACATTGTGCTGAATTC 1102

Qy   841 CGTACC 846
          ||||||
Db   1103 CGTACC 1108

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Qy   541  CTGCGAGAAGCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGTGTTGGGGAGAAACCA  600
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Db   803  CTGCGAGAAGCAGCCCAAGGGCAAGCACAAGCTCAATAAGGGGTGTTGGGGAGAAACCA  862

Qy   501  AACTTGCCTGAGTACAAAGTAGCGCCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT  660
          ||||.||||||||||||||||||||||||.|||||||.||||||| |||||| ||| |||
Db   863  AACTTGCCTGAGTACAAAGTAGCCGCCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT  922

Qy   661  GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCATGTGGCTGC  720
          ||||||||||||||||| ||||||||||||||||| ||||||||||| |||||||||
Db   923  GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCATGTGGCTGC  982

Qy   721  ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGGCCCGTGTGTGAGCACAGC...TTC  780
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Db   983  ACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGGACCCGTGTGTGAGCACAGC...TTC  1042

Qy   781  CCCAGCGTCTGTGACCTGGCCGTGGAGTCCTCTTCATCCTTGACATTGTGCTGAATTC  840
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Db   1043 CCCAGCGTCTGTGACCTGGCCGTGGAGTCCTCTTCATCCTTGACATTGTGCTGAATTC  1102

Qy   841  CGTACC  846
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Db   1103 CGTACC  1108
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Query Match          23.4%;  Score 761.2;  DB 14;  Length 3321;
Best Local Similarity  62.2%;  Pred. No. 2.2e-179;
Matches 1319;  Conservative  0;  Mismatches 706;  Indels  93;  Gaps  4;

Qy    1  ATGGCCGGCCATGCGGGGCCCTCCTGTGGGCGCCTCAGAACACTTCCTGGACACCATCGCCTACG  60
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Db    1  ATGGCCGGTTATGAAAGGATTACTGGCGGCACCATGGCCCATCCTGGACACCATCGCCACC  60

Qy   61  CGCTTCGACGGCACGGCACGCAGTAACTTCGTGCTGCTGGGCAACGCCCAGGTGGCGGGGGTCTTC  120
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Db   61  CGTTTTGACGGAACACATAGCAACTTCATCATCCTTGCCAATGCCCAGGTGGCTCAAGGGTTTC  120

Qy  121  CCGTGTCGTCACTGCTCTGATGGCTTCTCTGACCTCACGGGCTTCTCCCGGGCTGAGGTC  180
         |||||||| |||| |||||| ||||||| ||||||||||||||||||| |
Db  121  CCCATAGTCACTGTTCCGATGGCTTCTCTGCGAGCTTGTGATTTGGGTTGCCCGGAACTGAAGTC  180

Qy  181  ATGCAGCGGGGCTGTGCCGTGCTCGTCCTTATGGGCCACAGACCACAGATCGAGCTCGTCCGC  240
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Db  181  ATGCAGAAGAGTTGTAGCTGCAAGTTCTTATTTGGGTTGAAACCAATGAGCAACTGAATG  240

Qy  241  CAACAGATACCGGCAAGGCCCTGGACGACGCACAAGGAGTTCAAGGCTCAGCTCATCCTGTAC  300
         ||| ||||||||||||  |||||||||||||||||||| |||| ||| |||||| ||
Db  241  CTTCAAATAGAAAGTCACTGGAGGAGAAAAACAGATTCAAAGAGAAATTATGTTCTAC  300
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Qy   1381  AGCAGCCTCACCAGCGTGGGCTTCGGCAACGTGTCCGCCAACACGGACACCGAGAAGATC  1440
           ||||||||||||||||||||||| || ||| ||||| | ||| ||||||| | || ||||
Db   1288  AGCAGCCTCACCAGCGTGGGGTTTGGGAACGTCTCTGCTAATACAGATGCCAGAAAAGATC  1347

Qy   1441  TTCTCCATCTGCACCATGCTCATCGGGCCCCTGATGCACGCGGTGGTGTTTGGGAACGTG  1500
           |||||||||||||||| || || |||||||| || ||||||||| |||||| |||||||
Db   1348  TTCTCCATCTCCACCATGCTGATTGGTGCCCTTGATGCACGCGTTGGTGTTTGGAAACGTG  1407

Qy   1501  ACGGCCATCATCCAGCGCATGTACGCCCGCCGCTTCTGTACCACAGCCGCACGCGCCGAC  1560
           || || ||||| ||| ||||||| || | ||| || | || |||| ||  ||  || ||
Db   1408  ACAGCAATCATACAGAGGATGTACTCCAGATGGTCCCTCTATCACACTAGAACTAGGAT  1467

Qy   1561  CTGCGCGACTACATCCGCATCCACCGTATCCCCAAGCCCCTCAAGCAGCCACAGCTGGAG  1620
           |||  || || | |||| | |||| || || ||| ||||  | | | | ||  || ||
Db   1468  CTGAAAGATTTCATCCGTGCCATCACTTGCCCCAACAACTCAAGCAGAGGATGCTCGAA  1527

Qy   1621  TACTTCCAGCCACCTGGCCGTGAACAATGCCATGGCACCACCGAGCTGCTGCCAGAGC  1680
           || ||| ||  ||| || || ||| | | | || | |||| | | ||| ||||||
Db   1528  TATTTTCAAACAACCTGGTCAGTCAACAATGAAATAGATTCAAATGAGCTTTTGAAAGAC  1587

Qy   1681  CTCCCTGACGAGCTGCGCGCAGACATCGCCATGCACCTGCACAAGGAGGTCTGCAGCTG  1740
           | || | |||||| || |||   |||| | | |||| |||| | || |   || ||  |
Db   1588  TTTCCAGATGAACTGCGTTCTGACATCACTATGCACTTGAACAAGGAGATCTTACAGTTG  1647

Qy   1741  CCACTGTTTGAGGCGGCCAGCCGGCTGCCTCGCGGGCACTGTCTCTGGCCCTGCGGGCCC  1800
           | | ||||      || ||  || ||| |  || | | ||  ||  || ||  || |
Db   1648  TCCCTTTTTGAATGTGCCAGGCGGGGCTCCAGGTCTCTGTCTCTACACATCAAAACC  1707

Qy   1801  GCCTTCTGCACGCGCGGCGAGTACCTCATCCACCAAGGCGATGCCCGCAGGCCCCTCTAC  1860
           |  |||| ||| | | |  | |||| ||| |  | ||   || ||  ||||  ||  ||
Db   1708  TCTTTCTGCTCCGGGAGTATCTGCGTCAAGGGGATGCTTTGCAGGCCATCTAC  1767

Qy   1861  TTTGTCTGCTCTCCATGGAGGTGCTCAAGGGTGGCACCGTCTCTCGCCATCCTAGGG  1920
           || |  |||| |  ||||| ||| | | |  | || ||||   |||| || | ||  |
Db   1768  TTTGTATGCTCGGGCTCCATGGAAGTTCTTAAAGACAGCATGGTCGTGGCTATTCTTGGG  1827

Qy   1921  AAGGGCGACCTGATCGGCTGTGAGCTGCCCGGCGGGAGCAGGTGGTAAAGGCCAATGCC  1980
           || |  || |   |  |  || | |   ||| ||| ||| || || ||||  || ||
Db   1828  AAAGGGGATTAATTGGAGCAAATCTATCAATTAAGGACCAAGTGATCAAGACCAATGCA  1887

Qy   1981  GACGTGAAGGGCTGACGTACTGCGTCCTGCAGTGTCTGCCAGCTGGCCTGCACGAC  2040
           ||  | ||| |   || ||  || | | |||| |  |||| ||| |||| | |  ||
Db   1888  GATGTAAAGGGCTTTAACCTACTGTGATCTCCAGTGTATCATCCTCAAAGGACTCTTTGAA  1947

Qy   2041  AGCCTTGCGCTGTACCCCGAGTTTGCCCCGCGCTTCAGTCGGTGGGCCTCCGAGGGGAGCTC  2100
           || | |||| |  | ||  |||||| | | |||| | ||  || | |  |||| |||
Db   1948  GTGCTAGACCTTTACCCAGAATATGCTCACAAATTCGTGGAAGACATTCAGCGATGACCTC  2007

Qy   2101  AGCTACAACCTGGGTGCTGG  2120
           | |||||| || | ||
Db   2008  ACATACAACCTCCGAGAAGG  2027
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Search completed: October 2, 2003, 00:18:04
Job time :799 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2003, 15:33:20 ; Search time 5966 Seconds
(without alignments)
13248.099 Million cell updates/sec

Title: US-09-965-830-1_COPY_6_3257
Perfect score: 3252
Sequence: 1 atgccgccatgcgggcct.......aagaaggcacagggtctga 3252

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   EST:*
    1:   em_estba:*
    2:   em_esthum:*
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    8:   cm_htc:*
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   29:   gb_gss2:*

No.		Score					ID	Accession / Description
5		662.8	20.4	5	662	10	BE795800	BE795800 601590834
6		658.8	20.2	6	714	10	BE778330	BE778330 601463723
7		608.6	18.7	7	617	9	AW249035	AW249035 2820908.5
8	c	584.4	17.9	8	704	14	CD354565	CD354565 UI-M-GMO-
9	c	550.6	16.9	9	651	9	AL134774	AL134774 DKFZp5471
10		492	15.1	10	501	9	AW249298	AW249298 2821074.5
11		477	14.7	11	865	14	CD106245	CD106245 AGENCOURT
12		470	14.5	12	482	10	BE266788	BE266788 601190482
13		424	13.0	13	424	10	AI272282	AI272282 ap23c04.x
14		369.8	11.4	14	682	13	BQ444229	BQ444229 UI-M-EXO-
15		361	11.1	15	522	12	BI975332	BI975332 483675 MA
16	c	345	10.6	16	710	12	BQ045257	BQ045257 UI-CF-EN1
17	c	337.4	10.4	17	387	14	R35526	R35526 yg64e08.r1
18	c	335.2	10.3	18	502	10	BG082483	BG082483 H3076F11-
19		328.4	10.1	19	463	14	R73353	R73353 yl10e04.r1
20	c	315.6	9.7	20	572	14	CB055396	CB055396 NISC_J103
21		313	9.6	21	391	14	R13511	R13511 yf59c02.r1
22		305.8	9.4	22	765	13	BU291269	BU291269 603636076
23		305.6	9.4	23	328	9	AA325048	AA325048 EST27976
24	c	305	9.4	24	717	10	BG069378	BG069378 H3076F11-
25		301.4	9.3	25	1076	12	BM561167	BM561167 AGENCOURT
26		294.4	9.1	26	1115	12	BM547060	BM547060 AGENCOURT
27		284.2	8.7	27	351	14	R35105	R35105 yg59f09.r1
28		278.8	8.6	28	839	12	BI737339	BI737339 603357994
29		271.4	8.3	29	438	14	CB751495	CB751495 AMGNNUC:N
30		261.8	8.1	30	337	10	BF449484	BF449484 maa43d03.
31	c	259.8	8.0	31	909	13	BX391570	BX391570
32		258.8	8.0	32	924	14	CA454037	CA454037 AGENCOURT
33		256	7.9	33	878	13	BU170580	BU170580 AGENCOURT
34		255.8	7.9	34	615	13	CB579755	CB579755 AMGNNUC:N
35	c	246.6	7.6	35	635	10	BF589083	BF589083 nac29:06.
36		246	7.6	36	661	11	B1390873	B1390873 pgpln.pk3
37		242.8	7.5	37	4059	11	AK032438	AK032438 Mus muscu
38		242.2	7.4	38	749	13	BU707188	BU707188 UI-M-FRO-
39		242.2	7.4	39	784	13	RU707166	RU707166 UI-M-FRO-
40		239.6	7.4	40	815	13	BM948237	BM948237 UI-M-EGOp
41		236.8	7.3	41	853	13	BU164703	BU164703 AGENCOURT
42	c	234	7.2	42	558	9	AI450906	AI450906 ms26e01.x
43	c	232.6	7.2	43	315	13	BY363096	BY363096
44		228	7.0	44	926	13	BX327696	BX327696
45	c	227.8	7.0	45	475	9	AW082228	AW082228 xb64c03.x

ALIGNMENTS

RESULT 1
U69184
LOCUS   U69184   1114 bp   mRNA   linear   EST 27-OCT-1999
DEFINITION U69184 Soares infant brain 1NIB Homo sapiens cDNA clone 37299, mRNA
            sequence.
ACCESSION   U69184
VERSION   U69184.1 GI:2739408
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1114)
AUTHORS   Volorio,S., Simon,G., Repetto,M., Cucciardi,M., Banfi,S., Borsani
            ,G., Ballabio,A. and Zollo,M.
TITLE   Sequencing analysis of forty-eight human image cDNA clones similar
            to drosophila mutant protein
JOURNAL   DNA Seq. 9 (5-6), 307-315 (1998)
MEDLINE   99452388
PUBMED   10524757
COMMENT   Contact: Zollo, Massimo
            Telethon Institute of Genetics and Medicine
            Via Olgettina 58, Milan, MI 20132, Italy
            Email: zollo@tigem.it.
FEATURES   Location/Qualifiers
     source   1..1114
                     /organism="Homo sapiens"

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match	Length	DB	ID	Description
1	844.4	26.0	1114	14	U69184	U69184 U69184 Soar
2	802.4	24.7	896	12	BM452074	BM452074 AGENCOURT
3	783.4	24.1	4015	11	AK048629	AK048629 Mus muscu
4	675.6	20.8	862	13	BU187340	BU187340 AGENCOURT

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                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /map=":2q13"
                /clone="37299"
                /sex="female"
                /dev_stage="73 days post natal"
                /lab_host="DH10B (ampicillin resistant)"
                /clone_lib="Soares infant brain 1NIB"
                /note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
                I; Site_2: Hind III; 1st strand cDNA was primed with a Not
                I - oligo(dT) primer [5'
                AACTGGAAGAATTCGGCACGCCGG-AGGAA-TTTTTTTTTTTTTTTTTT 3'];
                double stranded cDNA was ligated to Hind III adaptors
                (Pharmacia). digested with Not I and directionally cloned
                into the Not I and Hind III sites of the Lafmid BA vector.
                Library went through one round of normalization. Library
                constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      189 a          370 c          368 g          187 t
ORIGIN

Query Match       26.0%;  Score 844.4;  DB 14;  Length 1114;
Best Local Similarity    99.9%;  Pred. No. 1.1e-148;
Matches 845;  Conservative   0;  Mismatches   1;  Indels   1;  Gaps   0;

Qy      1  ATGGCCGGCCATGCGGGGCCTCCTGGCGCTCCTGGAGCCTTCCTGGACCACCATCGCTACG  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245  ATGGCCGGCCATGCGGGGCCTCCTGGCGCCCCGCAGAACCACCTTCCTGGACCACCATCGCTACG  304

Qy     61  CGCTTCGACGGCACGCACGCCACAGTAACTTCGTGCTGGCAACGCCCAGGTGGCGGGGCCTCTTC  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305  CGCTTCGACGGCACGCACGCCACAGTAACTTCGTGCTGGCAACGCCCAGGTGGCGGGGCCTCTTC  364

Qy    121  CCCGTGGTCTACTGCTGCTGATGGCTTCTGTGACCTCACGGGTTCTCCCGGGCTGAGGTC  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365  CCCGTGGTCTACTGCTGCTGATGGCTTCTGTGACCTCACGGGTTCTCCCGGGCTGAGGTC  424

Qy    181  ATGCAGCGGGGCTGTGCCTGCTCCTTCCTTTATGGGCCAGCACCAGTGAGCTCGTCCGC  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425  ATGCAGCGGGGCTGTGCCTGCTCCTTCCTTTATGGGCCAGCACCAGTGAGCTCGTCCGC  484

Qy    241  CAACAGATCCGCAAGGCCCTGGACGCCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485  CAACAGATCCGCAAGGCCCTGGACGCCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC  544

Qy    301  CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGATGTATACCCATAAAGAATGAGAAA  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545  CGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGATGTATACCCATAAAGAATGAGAAA  604

Qy    361  GGGGAGGTGGCTCTTCTTCCTAGTCTCTCACAAGGACATCACCGAAACCAAGAACCGAGGG  420
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Db    605  GGGGAGGTGGCTCTTCTTCCTAGTCTCTCACAAGGACATCACCGAAACCAAGAACCGAGGG  664

Qy    421  GGGCCCGACAGATGGAAGGAACAGG-GTGTGCCCGGCCGATATGGCCGGCCACGATCC  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665  GGGCCCGACAGATGGAAGGAGAGGAGGACAGGTGGTGCCCGGCCGATATGGCCGGCCACGATCC  724

Qy    481  AAAGGCTTCAATGCCAACCGGCGGGCGGAGCCGGGCCGTGCTCCTACCACC-GTGCCGGGCAC  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725  AAAGGCTTCAATGCCAACCGGCGGGCGGAGCCGGGCCGTGCTCCTACCACCGTGCCGGGCAC  784

Qy    541  CTGCAAGCAGCAGCCAGGGCAAGCACCAAGCTCAATAAGGGGTGTTGGGGAGAAACCA  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    785  CTGCAGAAGCAGCAGCCAGGGCAAGCACAAGCTCAATAAGGGGTGTTGGGGAGAAACCA  844

Qy    601  AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    845  AACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT  904

Qy    661  GGGGCACTGAGAGCCCACCTGGATGCCTTCATCTGCTCGCCGCCACACTCTATGTGGCTGTC  720
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Db    905  GGGGCACTGAGAGCCCACCTGGATGGCCTTCATCTGCTCGCCGCCACACTCTATGTGGCTGTC  964

Qy    721  ACTGTGCCGACGGTGTGTGAGCACAGCAGCACGGGACGGAGCCCAGTGCGGCGGCCCCGGCCG  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    955  ACTGTGCCCTACACGCGTGTGTGAGCACAGCAGCACACGGGAGGCCCTTCATCGTTGACATTGTGCTGAATTTC  1024
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    781  CCCAGGTCTGTGACCTGGCCGGGAGGCGGAGGCCCTCTTCATCGTTGACATTGTGCTGAATTTC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1025  CCCAGGTCTGTGACCTGGCCGGGAGGCGGAGGCCCTCTTCATCGTTGACATTGTGCTGAATTTC  1084

Qy    841  CGTACC  846
           ||||||
Db   1085  CGTACC  1090
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RESULT 2
BM452074

```
LOCUS          BM452074              896 bp  mRNA  linear  EST 05-FEB-2002
DEFINITION     AGENCOURT_6397332 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:5492993
               5', mRNA sequence.
ACCESSION      BM452074
VERSION        BM452074.1  GI:18501114
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 896)
AUTHORS        NIH-MGC http://mgc.nci.nih.gov/.
TITLE          National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: ATCC
               cDNA Library Preparation: Life Technologies, Inc.
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL);
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               plate: LLAM12115 row: p  column: 18
               High quality sequence stop: 610.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5492993"
                     /tissue_type="retinoblastoma"
                     /lab_host="DH10B (phage resistant)"
                     /clone_lib="NIH_MGC_67"
                     /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT;
                     Average insert size 1.75 kb. Library constructed by Life
                     Technologies."
BASE COUNT      173 a          280 c          263 g          180 t
ORIGIN

Query Match       24.7%;  Score 802.4;  DB 12;  Length 896;
Best Local Similarity    95.2%;  Pred. No. 8.1e-141;
Matches 849;  Conservative   0;  Mismatches  41;  Indels   2;  Gaps   2;

Qy    292  ATCCTGTACCGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAG  351
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  ATCCTGTACCGGAAGAGCGGGCTCCCGTTCTGGTGTCTCCTGGATGTGATACCCATAAAG  60

Qy    352  AATGAGAAAGGGGAGGTGGCTCTTCTTCCTAGTCTCTCACAAGGACATCAGCGGAAACCAAG  411
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  AATGAGAAAGGGGAGGTGGCTCTTCTTCCTAGTCTCTCACAAGGACATCAGCGGAAACCAAG  120

Qy    412  AACCGAGGGGGGCCCCGACAGATGGAAGGAGGACAGGTGGTGCCCGGCCGATATGGCCGG  471
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  AACCGAGGGGGGCCCCGACAGATGGAAGGAGGACAGGTGGTGCCCGGCCGATATGGCCGG  180

Qy    472  GCACGATCCAAAGGCTTCAATGCCAACCGGCGGGCGGAGCCGGGCCGTGCTCCTACCACTG  531
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      181  GCACGATCCAAAGGCTTCAATGCCAACCGGCGGCGGGAGCCGGCCGTGCTCTACCACCTG  240
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy      532  TCCGGGCACCTGCAGAAGCAGCCAAGGCAGCACCAAGCTCAATAGGGGTGGTTGGG  591
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  TCCGGGCACCTGCAGAAGCAGCCAAGGCAAGCTCAATAGGGGGGTTTGGG  300

Qy      592  GAGAAAACCAAACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTG  651
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301  GAGAAAACCAAACTTGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTG  360

Qy      652  TTGCACTGTGGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACTCTCAT  711
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361  TTGCACTGTGGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTAT  420

Qy      712  GTGGCTGTCACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGAGCCCAGTGCCGCC  771
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Db      421  GTGGCTGTCACTGTGCCCTACAGCGTGTGTGAGCACAGCACGGAGCCCAGTGCCGCC  480

Qy      772  CCGGGCCGCCCAGCGTCTGTGACCTGGCCCTGGAGGTCCTTCATCCTTGACATTGTG  831
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481  CGGGGCCCCCCAGCGTCTGTGACCTGGCCCTGGAGGTCCTTCATCCTTGACATTGTG  540

Qy      832  CTGAATTCCGTACCACCATTCGTCGTCCAAGTCGTGTCGCCCAGGTGCGTTGCCCCAAAGTCC  891
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541  CTGAATTCCGTACCACCATTCGTCGTCCAAGTCGGCGCCAGGTGGTGTTGCCCCAAAGTCC  600

Qy      892  ATTGCCTCCACTACGTCACCACCTGGTTCCTGCTGGATGTCATCGGCAGCGCTGCCCTT  951
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Db      601  ATTTGCCTCCACTACGTCACCACCTGGTTCCTGCTGGATGTCATCGGCAGCGCTGCCCTT  660

Qy      952  GACCTGCTACATGCCTTCAAGGTCAACGTGCTACTTCGGGGCCCATCTGCTGAAGACGGTG  1011
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661  GACCTGCTACATGCCTTCAAGGTCAACGTGCTACTTCGGGGCCCATCTGCTGAAGACGGTG  720

Qy      1012 CGGCTGCTGCGCCCTGCTCGCCGGCTGGTTCCGGGGCGGTACTCGCCAGTAC-AGCGC  1070
                  |||||||||||||||||||||||||||| |||||||||||||||||||| |||||
Db      721  CGCCTGCTGCGCGCCCTGCTCGCCCGGCTGGTTCCGGGCCGGTACTCGCCAGAACAAGGCC  780

Qy      1071 CGTGGTGCTGACACTGCTCAT-GGCCGTGTTCGCCCTGCGCCCTGGTCGCCTCGCG  1125
                  |||||||||||||||||||| ||||||||||||| |||||||||||||||
Db      781  CGTGGGGCTGACACTGCTCATGGGCCCGTGTTCGCCCTGCGCCATTGGGCCCCCTGGC  840

Qy      1130 TCTGGTTTACATTGGCCAGCGGGGAGATCGAGCAGCGAGCAGCAACCGAGTCTGCC  1189
                  ||| | ||      ||    |    ||||| |      || |||| |||
Db      841  GTCTGGTTTACATTGCGCCCAAGCGGCGAGAACCAAGAGCAACCAAGGCAACCGAAATCCC  892
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RESULT 3
AK048629

LOCUS   AK048629   4015 bp   mRNA   linear   HTC 05-DEC-2002
DEFINITION   Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
               library, clone:C130090D05 product:ELK CHANNEL 3 (FRAGMENT) homolog
               [Rattus norvegicus], full insert sequence.
ACCESSION   AK048629
VERSION   AK048629.1 GI:26339459
KEYWORDS   HTC; CAP trapper.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
               Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
               prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374

Db   181 ...continued above

REFERENCE   (bases 1 to 4015)
  AUTHORS   (unassigned)

   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
               Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
               Sumi,N., Ishii,Y., Nakamura,Y., Hazama,M., Nishine,T., Harada,A.,
               Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
               Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
               Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,K., Kawai,J.,
               Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system-384-format
               sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
               Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
               Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
               Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
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               Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
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               Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
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               Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
               Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
               Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
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               Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
               Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
               Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
               Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
               Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
               and Hayashizaki,Y.
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
               Group Phase I & II Team.
  TITLE   Analysis of the mouse transcriptome based on functional annotation
               of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6 (bases 1 to 4015)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
               Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
               Hayashida,K., Hayatsu,N., Hiramoto,K., Hiramoto,T., Hircrane,T.,
               Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Kadowaki,T.,
               Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
               Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
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               Sogabe,Y., Tagami,T., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
               Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
               Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
               Physical and Chemical Research (RIKEN); Laboratory for Genome
               Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
               RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
               Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
               URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
               Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
               Encyclopedia Project of Genome Exploration Research Group in Riken
               Genomic Sciences Center and Genome Science Laboratory in RIKEN.
               Division of Experimental Animal Research in Riken contributed to
               prepare mouse tissues.
               Please visit our web site for further details.
               URL:http://genome.gsc.riken.go.jp/
               URL:http://fantom.gsc.riken.go.jp/

FEATURES   Location/Qualifiers
source   1..4015
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                /strain="C57BL/6J"
                /db_xref="FANTOM_DB:C130090D05"
                /db_xref="taxon:10090"
                /clone="C130090D05"
                /tissue_type="head"
                /clone_lib="RIKEN full-length enriched mouse cDNA library"
                /dev_stage="15 days embryo"
CDS   <1..3294
                /note="unnamed protein product; ELK CHANNEL 3 (FRAGMENT);
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                putative"
                /codon_start=1
                /protein_id="BAC33401.1"
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                CELAGFARTEVMQKSCSCKFLFGVETNEQLM:QIEKSLEEKVEFKGEIMFYKKNGAFF
                WCLLLDIVPIKNEKGDVVLFLASFKDITDTKVKITSEDKKEDRTKGRSRAGSHFLSAKE
                RSRAV.YHISGSLQRREKNKLKINNVFVDKFAFPEYKASDAKKSKFILLHFSTFKAG
                WDWLILLATFYVAVTVPYNVCFIGNEDLSTTRSTTVSDIAVEILFIDITLNFRTTYV
                SKSGQVIFEARSIC:HYVTTWFIIDLIAALPFDLLYAFNTVVSLVHLLKTVRLLRL:
                RLLQKLDRYSGHSTIVLILLMSMFALLAHWMACIWYIIGKMEREDNSLLKWEVGW.HF
                LGKRLESPYYGNNTLGPSIRSAYIAALYFTLSSLTSVGFGNVSANTDAEKIFSIC:M
                LIGAIMHIALVFGNVTAIIQRMYSRWSLYHTRTKDLKDFIRVHHLPQQLKQRMLEYFCT
                TWSVNNGIDSNELLKDFPDELRSDITMHLDKEILQLSLFECASRGCLRS.SLHIKISF
                CAPGEYLLRQGDALQAIYFVCSGSMEVLKDSMVLAILGKDLIGANLSIKDQVIKINA
                DVKALTYCDLQCIIIKGLFEVLGLYPEYAHKFVEDIQHDLTYN:REGHSSDVISRLSN
                KSTVSQAEPKGNGSINKRLPSIVEDEEEEVEEEETSLSPIYTRGSSVHSKKVQSN
                KTYLGLSLKQLASGTVPFHSPIRVSSANSPKTKOEADPPNHGRKKEKNLKVQI.SSLGS
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                ETKQQINKLNSEVTLLTQEVSQLGRDMRSIMQLLENILSPQQPSQFCSLHPTPMCPSR
                ESLQTRVSWSAHQPCLHLQAGGAHLYHGNVASGTWSVDPSLVGSSPQRTEAHHEONPAD
                SELHHSPNLDYSPSHCQVIOEGHLQFLRCISPHSDTTLTPLQSISATLSSSVCSSSET
                SIAHLVLPSRSREGSSTTHGPVSSFSLENLPGSWDREQMMSASSERLENEPVYVTSTAD
                VKDSKAINV"
BASE COUNT   1131 a   941 c   916 g   1027 t
ORIGIN

Query Match   24.1%;   Score 783.4;   DB 11;   Length 4015;
Best Local Similarity   62.8%;   Pred. No. 4.1e-137;
Matches 1321;   Conservative   0;   Mismatches 691;   Indels   93;   Gaps   3;

Qy   436 AAGGAGGACAGGTGGTGGCCGGCCGATATGGCCGGCACGATCCAAAGGCTTCAATGCC 495
                 || | | ||| | | | | | | |||| ||| | || ||
Db   412 GGAAGATAAAAAAGAAGAACAGAACCAAAGGAAGAATCAAGAGAGATCAAGAGGCCACTTGACTCA 475

Qy   496 AACCGGCGGGCGGAGCCGGCGGCCGTGCTCTACCACGTGTCCGGGCACCTGCAGAAGCAGCCC 555
                |||| || ||| || ||| || || | ||| | || || | || ||
Db   472 GCCCGGAGACGGAGCCGCAGCCGTGCTCTATCACACTCAGACAACCTTCAAAGAAGAAGAA 531

Qy   556 AAGGGCAAGCAAGCTCAATAAGGGGTGTTGGGGAGAAACCAAACTTGCCTGAGTAC 615
                ||| || | |||| || | | ||| | || | | || |||
Db   532 AAGAACAAATTGAAAATAAATAAAATAACGTGTTGTAGATAAACCAGCGTTCCAGAGTAT 591

Qy   616 AAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGTGGGCACTGAGAGCC 675
                || || |||| ||||| ||||||||| ||| |||||
Db   592 AAGGCTTCTGATGCAAGAAAGTCCAAGTTCATCCTGCTGCATTCAGCCACTTTCAAAGCT 651

Qy   675 ACCTGGATGGCTTCATCCTGCTCGCCACACTCTATGTGCCTGTCACTGTGCCCTACAGC 735
                |||| | | || |||| | | |||| | || |||| || || ||||| ||
Db   652 GGCTGGGACTGGCTGCTCATTTGCTGCAACGTTTTGTTGCTGCAACGGTCAGTGAC 711

Qy   735 GTGTGTGAGCACAGCACGGAGCCCAGTGCCGCCCGCCAGCCGCTGTGAC 795
                ||||||| | | | || || || | || || || ||||
Db   712 GTGTGTT---CATTGGCAATGAGGACCCTGTCCACCACCCGAGCACAACGGTCAGTGAC 768

Qy   796 CTGGCCCTGGAGGTCCTCTCATCCTGACATTGTGCTGAATTCGTACCACCATTCCTG 855
                || | ||||||| || |||||| || || | |||||| || || ||
Db   769 ATTGCAGTGGAGATACTGTTCATTATAGATTATTCTAAAATTTCCGAACAACTTATGTC 828

Qy   856 TCCAAGTCGGGCCAGTGGTGTTGTTGCCCCAAAGTCCATTTGCCTCCACTACGTCACCACC 915
                ||| ||||| | || | | | ||| || ||| | |||||||| | ||| || ||||||
Db   829 AGCAAGTCTGGCCAAGTTATCTTTGAAGCGAGATCCATTGCATTGCATTCTACTACGTCACCACC 888

Qy   916 TGGTTCCTGCTGATGTCATCGCAGCGCTGCCCTTGACCTGCTCTACATGCCTTCAAGGTC 975
                |||||| || ||| || || ||| |||| ||| ||| || | |||| || ||
Db   889 TGGTTCATCATTGATCTGATTGCTGCCCTTGACCTCCTGTAIGCTTATGCTTCAATGTC 948

Qy   976 AACCTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCCGCCTCCTGAAGACTGTTCGGCTC 1035
                | | || | ||| || || ||| ||| | | | | ||| ||| |||||
Db   949 ACAGTGGTGTCCCTCGTTCATCTCGTTCCTGAAGACTACAGCGGCCGCTGCTCATGGCC 1008

Qy   1036 CTTCGCGCGGCCGGACCGGTACTCGGCACTGGGTGCTGACACGGCCCGCCATGGCC 1095
                 ||| | ||| ||||| || || | || || | ||| |||||| || |
Db   1009 CTCCAGAAGCTGGACCGTTATTCTCAGCACAGTAGGTCCTCACCCTGCTCATCGCC 1066

Qy   1096 GTGTTCGCCTGCTGCTCGCGCACTGGGTGCTGCTGGTTTACATTGGCCAGCGGCGAG 1155
                ||||| | ||| || || | ||| | | || | | |||||| | ||||| ||
Db   1069 ATGTTTGCTCGTCGTTGCACACTGGATGATGCATGTGGTATAATCATTGGAAAAATGGAG 1128

Qy   1156 ATCGAGACAGCGAATCCGGAATCCGAGATTGGCTGGCTGCAGAATCGCCGCCGCCGA 1215
                  ||| || | ||| | || || || ||| || | ||||| || || ||||
Db   1129 AGGGAGGACAACAGCCTTCAAGTGGGAAGCGCGGTTGGCTTCATGAGCTGGGGAAGAGA 1188

Qy   1216 CTGGAGACTCCCTACTAACCTGGTGGGGCTCATGCAGCGGGGCTGT 1275
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Db   1189 CTGGAGACTCCCTACTAACCTGGTGGGGCTGAGTGCAGCGGGCTGT 1206

Qy   1276 AGTGACAACTGCAGCAGCAGGGAGGCCAACGGGGCAGGGCTGCTGGGCGGC 1335
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Db   1207 -------GGCAACAACACGCTGGGGGCC 1227

Qy   1336 CCGTCGCGCAGCGCCGCTACATCACCTCCCTACTTCGCAGCCTCAGCAGC 1395
                 ||| | || ||||| || | | | || || | | |||||| ||
Db   1228 CCATCCATCCGCAAGTGCCTATATTGCGGGCTAGTACTTCACTCGCAGCCTTCACAAGC 1287

Qy   1396 GTGGGCTTCGGCAACGTGTCGCGCAACGAGATCTTCTCAICTGACC 1455
                |||||| || || || ||| | || | || || |||| | | ||
Db   1288 GTTGGGTTTGGGAATGTGTCTGCTAACAGATGCAGAAGAATCTTCTCCATCTGCACC 1347

Qy   1456 ATGCTCATGCCGCCCCTGATGCACGGGTGTGTTGGGACCTGGTACGACGGGCCGCATCATCCAG 1515
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                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_67"
                /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT;
                Average insert size 1.75 kb.  Library constructed by Life
                Technologies."

BASE COUNT      146 a      273 c      264 g      174 t      5 others
ORIGIN

Query Match          20.8%;   Score 675.6;  DB 13;   Length 862;
Best Local Similarity  94.5%;  Pred. No. 5.6e-117;
Matches  763;   Conservative   0;   Mismatches  37;   Indels   7;   Gaps   6;

Qy   545 AGAAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTGGGAGAAACCAAACT 604
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 AGAAGCAGCCCAAGGCAAGCACAAGCTCAATAAGGGGTGTTGGGAGAAACCAAACT 60

Qy   605 TGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGTGGGG 664
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 TGCCTGAGTACAAAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGTGGGG 120

Qy   665 CACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTCACTG 724
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CACTGAGAGCCACCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTCACTG 180

Qy   725 TGCCCTACAGCGTGTGTGAGCACACAGCACGGGAGCCAGTGCCGCCCGGCCGGCCCCA 784
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGCCCTACAGCGTGTGTGAGCACACAGCACGGGAGCCAGTGCCGCCCGGCCGGCCCCA 240

Qy   785 GGGTCTGTGACCTGGGCCCGTGAGCTCCTCTTCATCCTTGACATTGTGCTGAATTGTCCGTA 844
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCGTCTGTGACCTGGGCCCGTGAGCTCCTCTTCATCCTTGACATTGTGCTGAATTGTCCGTA 300

Qy   845 CCAATTCGTCTCCAAGTCGGGCCAGTGGTGTTGCCCCAAAGTCCATTTGCCTCCACT 904
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCAATTCGTCTCCAAGTCGGGCCAGTGGTGTTGCCCCAAAGTCCATTTGCCTCCACT 360

Qy   905 ACGTCACCACCTGGTTCCTGCTGGATGTCATCGCAGCCGCCATCGCAGCCGCCATCGCTACACATG 964
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ACGTCACCACCTGGTTCCTGCTGGATGTCATCGCAGCCGCCATCGCAGCCGCCATCGCTACACATG 420

Qy   965 CCTTCAAGGTCAACGTGTACTTCGGGGCCCATCGTGCTGGAAGAGTGCCGCGTCGCGCTCGCCGCC 1024
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCTTCAAGGTCAACGTGTACTTCGGGGCCCATCGTGCTGGAAGAGTGCCGCGTCGCGCTCGCCGCC 480

Qy  1025 TGCTGGCCTGCTTCCGGGGCGTGGACCGGTGGACTGCAGTACAGCG-CCGGTGGTGCTGACA 1083
         |.||||||||||||||||||||||||||||||||||||||||| |.|||||||||||||||
Db   481 TGCTGCGGCCTGCTTCCGGGGCGTGGACCGGTGGACTGCGACANACAAGCGCCCGGTGGTGCTGACA 540

Qy  1084 CTGGCCATGGCCGTGTTCCGGCTGCCCTGCTCGCGCACTGGGTCGCCT-CCGTCTCGGTTTACAT 1142
         ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db   541 CTGGCCATGGCCGTGTTCCGGCTGCCCTGCTCGCGCACTGGGTCGCCTCCGGTCTCGGTGTTTACAT 600

Qy  1143 TGGCCAGC-GGGAGATCGAGAGCAGCAGCAATCCGAGCTGCCT-GAGATTGGCIGGCTGCAG 1200
         ||||||||| ||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   601 TGGCCAGCNGGGAGATCGAGAGCAGCAGCAATCCGAGCTGCCTNGAGATTGGCTGGCTGCAG 660

Qy  1201 GAGCTGGCCGACTGGAGACTCCCTACTACCTGGTGG--CCGGAGGCCAGCTGGAG 1258
         |||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db   661 GAGCTGGCCGACTGGAGACTCTANTTACTGGGGGGCCGGGAGGCCAGCTGGAG 720

Qy  1259 GGAACAGC-TCCGGCCAGAGTGACAACTGCAACAACGGGGACGGGG 1317
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Db   721 GGAACAGCTTCCGGCCAGAGTGACAACTGCAACAACGGGACGGGG 780

Qy  1318 CTGGAGCTGCTGGGCGGCCCGTCGCTG 1344
         |   ||| ||||||||| ||||| ||||
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Qy  1516 CGCATGTACGCCCGCGCCTTTCTGTACCACAGCCGCACGCGCGACCTGCGCGACTACATC 1575
         |||||||||| | ||| || | |||||||| | || |||| | || ||| ||||| ||||
Db  1408 AGAATGTACTCTAGATGGAGCCTGTACCACACTAGAACCAAGGACCTAAAAGACTTCATC 1467

Qy  1575 CGCATCCACCGTATCCCCAAGCCCCTCAAGCAGCCCATGCTGGAGTACTTCCAGGCCACC 1635
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Db  1468 CGTGTGCACCACCTGCCCCCAGCAACTCAAGCAGCGATGCTGCTGAGTACTTTCAGACAACT 1527

Qy  1636 TGGGCGGTGAACAATGGCATCGACACCACCGAGTGCTGCTGACGAGCCTCCCTGACGAGCTG 1695
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Db  1528 TGGTCAGTCAACAATGGGGATAGAATTCAAATGAGCTTTAAAAGACTTTCCAGATGAGCTG 1587

Qy  1696 CGGCGCAGACATGCCCATGCCACTGCACAAGGAGAGTCCTGCAGCTGCCACTGTTTGAGGCG 1755
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Db  1588 CGCTCTGACATCACAATGCATCTGGACAAGGAGATCTTACAGCTGCTGCCCGTTCGAATGT 1647

Qy  1756 GCCAGCCGGCGGCTGCCTGCGGGACACTGCTTCTGGCCTGCTGCCCGGCCTTCTGCACGGCG 1815
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Db  1648 GCCAGCCGGGGGGCTGCCTCAGGTCTTCTGTCTCTCCACAATTAAAACCTCCTTTTGTGCTCCA 1707
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RESULT 4
BU187340
LOCUS       BU187340               862 bp    mRNA       linear   EST 04-SEP-2002
DEFINITION  AGENCOURT_7888553 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6140620
            5', mRNA sequence.
ACCESSION   BU187340
VERSION     BU187340.1  GI:22701324
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 862)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13459  row: i  column: 05
            High quality sequence stop: 522.
FEATURES             Location/Qualifiers
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Db   781 GGTCTGGAACCTGCTGGGGCGGGGCCCG 807

RESULT 5
BE795800
LOCUS   BE795800   766 bp   mRNA   linear   EST 20-SEP-2000
DEFINITION   601590834F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944793 5',
             mRNA sequence.
ACCESSION   BE795800
VERSION   BE795800.1 GI:10216998
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
             Plate: LLCM802 row: 3 column: 10
             High quality sequence start: 5
             High quality sequence stop: 763.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:3944793"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCAGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit.
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT   122 a   275 c   234 g   135 t
ORIGIN

Query Match   20.4%;   Score 562.8;   DB 10;   Length 766;
Best Local Similarity 96.4%;   Pred. No. 1.4e-114;
Matches 744; Conservative 0; Mismatches 17; Indels 11; Gaps 6;

Qy 2219 CGGTCTCCCCAGCCGTGATGAGCCCTCCAGCCCCCGCTGTCCCCTGGCTGCACCT 2278
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Db   4 CGGTCTCCCCAGCCGTGATGAGCCCTCCAGCCCCCGCTGTCGCCCTGGCTGCACCT   63

Qy 2279 CCTCATCCTCAGTGCCAAGCTGCTATCCCCACGTCGAACAGCACCCCGGCCCTCGTCTAG 2338
          |||||||||||||||||||||||||||||||||||| |||||||| |||||
Db   64 CCTCATCCTCAGTGCCAAGCTGCTATCCCCACGTCGAACAGCACCCCGGCCCTCGTCTAG 123

Qy 2339 GTGGCAGAGGGAGGCCAGGCAGGGCAGGGCTTTGAAGGCTGAGGCTGGCCCCTCTGGTC 2398
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   124 GTGGCAGAGGGAGGCCAGGCAGGGCAGGGCTTTGAAGGCTGAGGCTGGCCCCTCTGGTC 183

Qy 2399 CCCCACGGGGCCCTAGAGGGGCTACGGCTGCCCCCCCATGGAATGTGCCCCCAGATC 2458
          ||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db   184 CCCCACGGGGCCCTAGAGGGGCTACGGCTGCCCCCCCATGGAATGTGCCCCCAGATC 243

Qy 2459 TGAGCCCCCAGGGTAGTAGATGGCATTGAAGACGGCGTGTGGCTCGGACCACCCAAGTTCT 2518
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Db   244 TGAGCCCCCA-GGTAGTAGAGGGCAGTCTGGCCGGAATGTGAGCAGCCCCTCCCCTGGACCAGAGA 302
           |||||||||| ||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Qy   256 CTTTCGCGGTGGGCCAGTCTGGCCCGGAATGTAGCAGCCCCCTCCCCCTGGACACACTGGACA 362
Db   303 CTTTCGCGGTGGGCCAGTCTGGCCCGGAATGTAGCAGCCCCCTCCCCCTGGACACACTGGACA 362

Qy   2579 GCGGCCTGCTCACTGTTCCCCATGGGCCAGCAGTGTCAGCAGCAAGGAACACAGACACTGGACA 2638
Db   363 GCGGCCTGCTCACGGTTCCCCATGGGCCAGCAGTGTCAGCAGCAAGGAACACAGACACTGGACA 422

Qy   2639 AGTTCGGCAGGCCGTGACAGAGCGTGCTCAGAGCAGTGCTGCAGATGCGGGAAGGATGC 2698
Db   423 AGTTCGGCAGGCCGTGACAGAGCGTGCTCAGAGCAGTGCTGCAGATGCGGGAAGGACTGC 482

Qy   2699 AGTCACTTCGCCAGCTGTCCTGGCGTTGTCCTGTCCTGGCCCCACCAGGGAGGGTCCGTGCCCTC 2758
Db   483 AGTCACTTCGCCAGCTGTCCTGGCGTTGTCCTGTCCTGGCCCCACCAGGGAGGGTCCGTGCCCTC 542

Qy   2759 GGGCATCGGGAGAGGGGCCGTGCCAGCAGCACCTCCGGGCTTCTGCAGCTCTGTGTG 2818
Db   543 GGGCATCGGGAGAGGGGCCGTGCCAGCAGCACCTCCGGGCTTCTGCAGCTCTGTGTG 602

Qy   2819 TGGACACTGGGCATCCTCCTACTGGCTGCAGCCCCAGGTGGCTCTGTCTGAGTGGGA 2878
Db   603 TGGACACTGGGCATCCTCCTACTGGCTGCAGCCCCAGGTGGCTCTGTCTGAGTGGGA 661

Qy   2879 CTTGGCCCCACCCTGTCCGGGGCC-CCTCCCCATGGCACCCTGGCCCTGGGGTCCCC 2938
Db   662 CTTGG-CCCACCCTGTCCGGGGCCTCCTCCC---TCATGCACCTGGCCTGGGGTCCAC 715

Qy   2939 CAGCGTCTCAGAGCTCCCCCTGGCCTCGAGCCACAGCTTTCTGGACCTCCAC 2990
Db   716 CAGCGTCTCAGAGCTCGCCCTGGCTCGAG---CACAGCTTTCTGGACTTCCAC 764

RESULT 6
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LOCUS   BE778330   714 bp   mRNA   linear   EST 20-OCT-2000
DEFINITION   601463723F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867076 5',
             mRNA sequence.
ACCESSION   BE778330
VERSION   BE778330.1 GI:10199528
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 714)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-r@mail.nih.gov
             Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM9612 row: n column: 05
             High quality sequence stop: 691.
FEATURES   Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_67"
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                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb.   Library constructed by Life
Technologies."

BASE COUNT   133 a   227 c   210 g   144 t
ORIGIN

Query Match
Best Local Similarity   99.3%;
Matches 703;   Conservative 0;   Mismatches 4;   Indels 1;   Gaps 4;

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Qy   377  TCCTAGTCTCTCACAAGACATCAGCGAAACCAAGAAACCGAGGGGCCCGACAGATGGA  436
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Db     1  TCCTAGTCTCTCACAAGACATCAGCGAAACCAAGAAACCGAGGGGCCCGACAGATGGA   60

Qy   437  AGGAGACAGGTGGTGGCCGGCCGCCGGCCGGATCAAGGCTTCAATGCCA  496
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  AGGAGACAGGTGGTGGCCGGCCGCCGGCCGGATATGGCCGGCACGATCCAAGGCTTCAATGCCA  120

Qy   497  ACCGGCGGCGAGCCGGCCGGCCGTGCTCTACCACCTGTCCGGGCACCTGCAGAAGCAGCCCA  556
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  ACCGGCGGCGAGCCGGCCGGCCGTGCTCTACCACCTGTCCGGGCACCTGCAGAAGCAGCCCA  180

Qy   557  AGGGCAAGCACACAAGCTCAATAAGGGGGTGTTTGGGGAGAAACCAAACTTGCCTGAGTACA  615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  AGGGCAAGCACACAAGCTCAATAAGGGGGTGTTTGGGGAGAAACCAAACTTGCCTGAGTACA  240

Qy   617  AAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGTGGGGCACTGCAGAGCCA  676
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  AAGTAGCCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGTGGGGCACTGCAGAGCCA  300

Qy   677  CCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCGCTCACTGTGCCCACAGCG  735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  CCTGGGATGGCTTCATCCTGCTCGCCACACTCTATGTGGCGCTCACTGTGCCCACAGCG  360

Qy   737  TGTGTGGAGCACAGCACGGGAGCCAGTGCCGCCGCCGCCCAGGGTCTGTGACC  796
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Db   361  TGTGTGGAGCACAGCACGGGAGCCAGTGCCGCCGCCCCCAGCGTCTGTGACC  420

Qy   797  TGGCCGTGG-AGGTCCCTTCATCCTTGACATTGTGCTGAATTCCGTACCACATTCGTG  855
          |||| |||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  TGGCCGTGGCAGGTCCCTTCATCCTTGACATTGTGCTGAATTCCGTACCACATTCGTG  480

Qy   856  TCCAAGTCGGCCCAGGTGGTGTTTGCCCCAAAGTCCATTTGCCTCCACTACGTCACCACC  915
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  TCCAAGTCGGCCCAGGTGGTGTTTGCCCCAAAGTCCATTTGCCTCCACTACGTCACCACC  540

Qy   916  TGGTTCCTGCTGGATGTCATCGCAGCGCCGCCCTTGACCTCTACAGCCTCAATGCCT  975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  TGTTCCTGCTGGATGTCATCGCAGCGCCGCCCTTGACCTCTACAGCCTCAATGCCT  600

Qy   976  AACGTGTACTTCGGGGCCCATCTGCTGAAGACGGTGCGCCTGCGCCTGCTGCTGAAGACGG  1035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  AACGTGTACTTCGGG-CCATCTGCTGAAGACGGTGCGCCTGCGCCTGCTGCTGAAGACGG  659

Qy  1036  CTTCCGGCGACCGGTACTCGCAGTA-CAGCGCCGTGGTGCTGAC  1082
          ||| |||| ||||||||||||||||| ||||||||||||||||
Db   660  CTTACGCGG-TGGACCGGTACTCGCAGTACCAGCGCCGTGGTGCTGAC  706
```

RESULT 7
AW249035
LOCUS   AW249035   617 bp   mRNA   linear   EST   07-JAN-2000
DEFINITION   2820908.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820908 5',
             mRNA sequence.
ACCESSION   AW249035
VERSION   AW249035.1   GI:6592028
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 617)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)

FEATURES   Location/Qualifiers
     source   1..617
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820908"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT   101 a   221 c   187 g   108 t
ORIGIN

Query Match
Best Local Similarity   99.3%;   Score 608.6;   DB 9;   Length 617;
Matches 511;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

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Qy  2431  CCCATGCCATGGAATGTGCCCCCAGATCTGAGCCCCAGGTAGTAGATGGCATTGAAGAC  2490
          | |  |   ||||||| |||||||||||||||||||||||||||||||||||||||||||
Db     3  CACGAGGCATGGAATGTGCCCCCAGATCTGAGCCCCAGGTAGTAGATGGCATTGAAGAC   52

Qy  2491  GGCGTGGCTCGGACCAGCCCAAGTCTTCTTCCGCGTGGCCCAGTCGTCGGCCCGGAATGT  2550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    63  GGCGTGGCTCGGACCAGCCCAAGTTCTTCTTCCGCGTGGCCCAGTCGTCGGCCCGGAATGT  122

Qy  2551  AGCAGCAGCCCCTCCCTGGACCAGAGAGCGGCCTGCTCACTGTTCCCATGGGCCCAGC  2610
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   123  AGCAGCAGCCCCTCCCTGGACCAGAGAGCGGCCTGCTCACTGTTCCCATGGGCCCAGC  182

Qy  2611  GAGGCAAGAACACAGCACACTGACAAGCTTCGGCAGGCGGTGACAAGAGTGTCAGAG  2670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   183  GAGGCAAGAACACAGCACACTGACAAGCTTCGGCAGGCGGTGACAAGAGTGTCAGAG  242

Qy  2671  CAGGTGCTGCAGATGCGGAAGGACTCGAGTCACTCGCAGCCTGTGCAGTCCAGCCAGC  2730
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   243  CAGGTGCTGCAGATGCGGAAGGACTCGAGTCACTCGCAGCCTGTGCAGTCCAGCCAGC  302

Qy  2731  GCGCCCCACAGGGAGGTCCGTGCCCTCGGGCATCGGGAGAGGGGCCGTGCCCAGCCAGC  2790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   303  GCGCCCCACAGGGAGGTCCGTGCCCTCGGGCATCGGGAGAGGGGCCGTGCCCAGCCAGC  362

Qy  2791  ACCTCGGGCTTCTGCAGCCTCTCGTGTGTGACACTGGGGCATCCTCCTACTGCCTGCAG  2850
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   363  ACCTCGGGCTTCTGCAGCCTCTCGTGTGTGACACTGGGGCATCCTCCTACTGCCTGCAG  422

Qy  2851  CCCCCAGCTGGCTCGTCTTCTTGAGTGGACTTGGCCCACCTCGTCGGGGCCTCCCC  2910
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   423  CCCCCAGCTGGCTCGTCTTCTTGAGTGGACTTGGCCCACCCTCGTCGGGGCCTCCCC  482
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Qy   2911 CTCATGGCACCCTGGCCCTGGGGTCCCCAGGAGCCTCAGAGAGCCTGGCCTCGAGCC 2970
          |||||||||||||||||||||||||||||||| |||||||| |||||||||||..||
Db    483 CTCATGGCACCCTGGCCCTGGGGTCCCCAGGCGTCAGAGAGCCTCAGAGAGCCTGGCCTCGAGCC 542

Qy   2971 ACAGCTTTCTGGACCTCCACCTCAGACTCAGAGCCCCTGCCTCAGGAGACCTCTGCTCT 3030
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    543 ACAGCTTTCTGGACCTCCACCTCAGACTCAGAGCCCCTGCCTCAGGAGACCTCTGCTCT 602

Qy   3031 GAGCCCCAGCACCCCT 3045
          ||||||||||||||||
Db    603 GAGCCCCAGCACCCCT 617

Qy   1661 CCACCGAGCTGCTCAGAGCCTCCCTGACGAGCTGCGGCAGCATGGCCATGCACCTGC 1720
          ||| |||||||||||||||||||||||||| |||||||| ||||||||||||||||||
Db      1 CCACTGAGCTGCTGCAGAGCCTCCCTGACGAGCTTCGTCCAGACATCGGCCATGCACCTGC 60

Qy   1721 ACAAGGAGGTCCTCGAGCTGCCCACGTGTTTGAGGCGGCCAGCCGGCCGGTGCTCGGGCCAC 1780
          |||||| ||||||||||||||||||| |||||||||| |||||||||||||.||||||||||
Db     61 ACAAGGAAGTCCTCGAGCTGCCCCAGCTGGCGGCCCGGCCGGTGCTGGGCCGCTGCCTCGGGCGGC 120

Qy   1781 TGTCTCTGGCCCTGCGGCCCTTCTGCAGCGGGAGTACCTCATCCATCCACCAAGGCG 1840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||::::
Db    121 TGTCCTGGCCCTGAGGCCGGCGGCCTTCGCACGCGGGAGTACCCTCATTCACCAAGGCG 180

Qy   1841 ATGCCCTGCAGGCCCTTCTACTTTGTCTGTCGGCTCCATGGAGGTGCTCAAGGGTGCA 1900
          |||||||||||||||||||::||||||| ||||||||||||||||||||||||||||||
Db    181 ATGCTCTCCAGGCCCTCTATTTGTCTGTCGGGTTCCATGGAGGTCCATGGAGGTGCA 240

Qy   1901 CCGTGCTCGCCATCCTAGGGAAGGGCACCTGATGGCTGTGAGCCGCGGCGGGAGC 1960
          ||||||||||||||||||||| ||||||||| |||| ||||||||||| ||||||
Db    241 CCGTGCTCGCCATCCTAGGGAAGGGCACCTGATGGCTGTGAGCCGCGGGGAAC 300

Qy   1961 AGGTGGTAAAGGCCAATGCCGACGTGAAGGGGCTGACGTACTGCGTCCTCGCAGTGTGC 2020
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Db    301 AAGTAGTGAAGGCCAATGCCAATGGCTGAGACGTGAAGGGGCTGACGTACTGCGTCCTCACAGTGTCTGC 360

Qy   2021 AGCTGGCTGGCTGCGACGACAGCCTTGGCCGTTGCCCCGCGTTCAGTC 2080
          |||||| |||||||||||||||||||| ||||| |||||| ||||||||
Db    361 AGTTGGCTGGGCTGCATGGAGCCGTGGCTGCTCGTGTACCCTGAGTTTGCCCCGCTTTAGCC 420

Qy   2081 GTGGCTCCGAGGGGAGCTCAGTCAACCTGGGTGCTGGGGGAGGCTCTGCAGAGGTGG 2140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTGGCCTCCGAGGGGAGCTCAGTCAACCTGGGAGGTGGTGGAG.CTGCGGAGGTGG 480

Qy   2141 ACACCAGCTCCCTGAGCGGGACAATACCCTTATGTCCACGGTGGAGGAGAAGGAGACAG 2200
          |||||||||||||||||||||||||:|||:||||||||||||||||||||||||||||||
Db    481 ATACCAGCTCCCTGAGTGGTGACAACACCCTCATGTCCCACTGGAGGAGAAGGAGACAG 540

Qy   2201 ATGGGGAGGAGGGCCCCCAGGGTCTCCCCAGCGTGATGAGCCCCTGCCAGCCCCTGC 2260
          ||||||||| | |||||||||| ||||||||||||||||||||||||:: ||||||||
Db    541 ATGGGGAGGACGGCACCACCGGTCTCACCAGCCCCAGCAGATGAGCCCCTCCAGTCCCCTGC 600

Qy   2261 TGTCCCCGGCTGCACCTCCTCATCCTCAGCTGCCAAGCTGCTATCCCCAGGTCGAACAG 2320
          |||| || ||||||||||||| |||||| |||||||||||||||||||||||||||||||
Db    601 TGTCGCCCGGCTGTACCTCCTCCTCCAGCCGCCAAACTACTCTCCCCACGTCGAACTG 660

Qy   2321 CACCCCGGCCTCGTCTAGGTGCAGAGGGAGGGCCAGGAGGCCAGGGCA 2364
          || ||||| ||||:|||||||||||||||::|| ||||||||
Db    661 CGCCCGGCCGAGGTTGGGTGCAGAGGGCGGCCAAGTAGGGCA 704
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RESULT 8
CD354565

LOCUS   CD354565   704 bp   mRNA   linear   EST 29-MAY-2003
DEFINITION   UI-M-GMO-cgd-j-0;-0-UI.rl NIH_RMAP_GMC Mus musculus cDNA clone
               IMAGE: 30361272 5', mRNA sequence.
ACCESSION   CD354565
VERSION   CD354565.1   GI:31147066
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 704)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r3mail.nih.gov
               Tissue Procurement: Dr. Jim Lin, University of Iowa
               cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
               cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
               DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
               Clone Distribution: Distribution information can be found at
               http://genome.uiowa.edu/distribution/mousefi.html
               This clone was contributed by the Brain Molecular Anatomy Project
               (BMAP)
               Seq primer: pYX-5.
FEATURES   Location/Qualifiers
     source   1..704
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE: 30361272"
                     /tissue_type="whole brain"
                     /dev_stage="1, 5 and 15 days newborn"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_ib="NIH_BMAP GMO"
                     /note="Organ: Brain; Vector: pYX- Asc: Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bocaldo. Lennon and Soares. Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel.First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site.Double strand cDNA was size
                     selected according to mRNA size fraction,ligated with EcoR
                     I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is CGAACTGAAT. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."

BASE COUNT   126 a   226 c   219 g   133 t
ORIGIN

Query Match   17.9%;   Score 582.4;   DB 14;   Length 704;
Best Local Similarity   89.2%;   Pred. No. 1.8e-99;
Matches 628;   Conservative   0;   Mismatches 76;   Indels   0;   Gaps   0;

RESULT 9
AL134774

LOCUS   AL134774   651 bp   mRNA   linear   EST 25-FEB-2000
DEFINITION   DKF2p547I2290_r1 547 (synonym: hfbr1) Homo sapiens cDNA clone
               DKF2p547I2290 5', mRNA sequence.
ACCESSION   AL134774
VERSION   AL134774.1   GI:6602961
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 651)
  AUTHORS   Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
  TITLE   EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann
               ,S.)
  JOURNAL   Unpublished
COMMENT   Contact: Poustka A.J.
               Department Lehrach
               Max-Planck-Institute for Molecular Genetics
               Ihnestrasse 73, 14195 Berlin, Germany
               Tel: +49-30-84131623
               Fax: +49-30-84131128

DEFINITION   2821074.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821074 5',
              mRNA sequence.
ACCESSION   AW249298
VERSION   AW249298.1 GI:6592291
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 501)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT   Other_ESTs: 282:074.3prime
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
              Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
              Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
              project Clone distribution: MGC clone distribution information can
              be found through the I.M.A.G.E. Consortium/LLNL at:
              www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
              Scores: PHRED from University of Washington Genome Center. Vector
              Trimming: cross_match from University of Washington Genome Center
              PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
              Drosophila Genome Project. University of Washington Genome Center:
              http://www.genome.washington.edu.
              Plate: LLCM5 row: N column:19
              High quality sequence stop: 500.
FEATURES   Location/Qualifiers
     source   1..501
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2821074"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT   98 a   182 c   142 g   79 t
ORIGIN

Query Match   15.1%; Score 492; DB 9; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.7e-82;
Matches 492;   Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1263 CAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCGAGGCCAACGGGACGGGGCTGGA 1322
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Db   10 CAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCGAGGCCAACGGGACGGGGCTGGA 69

Qy   1323 GCTGCTGGGGCCGGGCCCGTCGCGTCGCGCCAGCGCCTACATCACCTCCCTCACTCAG 1382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   70 GCTGCTGGGGCCGGGCCCGTCGCGTCGCGCCAGCGCCTACATCACCTCCCTCACTCAG 129

Qy   1383 CAGCTCACCAGCGTGGGCTTCGGCAACGTGTCCGGCAACACACCGACACCGACAAGATCTT 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   130 CAGCTCACCAGCGTGGGCTTCGGCAACGTGTCCGGCAACACACCGACACCGACAAGATCTT 189

Qy   1443 CTCCATCTGCACCATGCTCATCGGCATGGATGCCTTCA 1502
          ||||||||||||||||||||||||||||||||||||||
Db   190 CTCCATCTGCACCATGCTCATCGGCATGGATGCCTTCA 249

Qy   1503 GGCCATCATCCAGCCAGCCATGTACGCCCGCGCCTTTCTGTACCACAGCCGCACGCCGACCT 1562
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   250 GGCCATCATCCAGCCAGCCATGTACGCCCGCGCCTTTCTGTACCACAGCCGCACGCCGACCT 309

RESULT 10
AW249298
LOCUS   AW249298   501 bp   mRNA   linear   EST 07-JAN-2000

Left column:

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Qy   1563 GCGGGACTACATCCGGATCATCCACCGTATCCCCAAGCACCCCTCAAGCAGCAGCATGCTGGAGTA 1622
          ||||||||||||||||| ||||||||||||||||||||||| |||||||||||| |||||||||| |
Db    310 GCGGGACTACATCCGGATCATCCACCGTATCCCCAAGCACCCCTCAAGCAGCAGCATGCTGGAGTA 369

Qy   1623 CTTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACCGAGCTGCTGCAGAGCCT 1682
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    370 CTTCCAGGCCACCTGGCGGTGAACAATGGCATCGACACCGAGCTGCTGCAGAGCCT 429

Qy   1683 CCCTGACGAGCGCGGCGGCCGCAGACATCGCCATGCGCATGCGCAAGGAGGTCCTGCAGCTGCC 1742
          |||||||||||||||||| ||||||||||||||||||||||||||||| |||||||||||||||
Db    430 CCCTGACGAGCGCGGCGGCCGCAGACATCGCCATGCGCATGCGCAAGGAGGTCCTGCAGCTGCC 489

Qy   1743 ACTGTTTGAGGC 1754
          |||||||||||
Db    490 ACTGTTTGAGGC 501
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RESULT 11
CD106245

LOCUS   CD106245   865 bp   mRNA   linear   EST 15-MAY-2003
DEFINITION AGENCOURT_13980050 NIH_MGC_179 Homo sapiens cDNA clone
           IMAGE:30368984 5', mRNA sequence.
ACCESSION CD106245
VERSION   CD106245.1 GI:30759419
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 865)
  AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Dr. Michael Brownstein
           cDNA Library Preparation: Invitrogen Corp
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: NDAM432 row: k column: 09
           High quality sequence stop: 548.
FEATURES   Location/Qualifiers
     source   1..865
                  /organism="Homo sapiens"
                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:30368984"
                  /tissue_type="pituitary"
                  /lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
                  /clone_lib="NIH_MGC_179"
                  /note="Organ: brain; Vector: pCMV-SPORT6.1; Site_1: EcoRV
                  (destroyed); Site_2: NotI; Library is oligo-dT primed and
                  directionally cloned (EcoRV site is destroyed upon cloning
). Average insert size 1.1 kb. Library was constructed by
                  (Invitrogen). Note: this is a NIH_MGC Library."
BASE COUNT   163 a   300 c   235 g   164 t   3 others
ORIGIN

Query Match   14.7%; Score 477; DB 14; Length 865;
Best Local Similarity 100.0%; Pred. No. 1.2e-79;
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   2776 CCGTGCCAGCCAGCACCTCCGGCTTCTGCAGCCTCTGTGTGTGGACACTGGGGCATCC 2835
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Db      1 CCGTGCCAGCCAGCACCTCCGGCTTCTGCAGCCTCTGTGTGTGGACACTGGGGCATCC 60

Qy   2836 TCCTACTGCCTGCAGCCCCAGCGTCGGCTGTCTTGAGTGGGACTTGGCCCACCCTCGT 2895
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCCTACTGCCTGCAGCCCCAGCGTCGGCTGTCTTGAGTGGGACTTGGCCCACCCTCGT 120
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Right column:

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Qy   2896 CCGGGGCCTCTCCCTCCCATGGCACCCTGGCCTCGGGGTCCCCAGCGTCTCAGAGCTCC 2955
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCGGGGCCTCTCCCTCCCATGGCACCCTGGCCTCGGGGTCCCCAGCGTCTCAGAGCTCC 180

Qy   2956 CCCTGGCCTCGAGCCACCAGCTTTCTGGACCTCAGACTCAGAGCCCCTGCCTCA 3015
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCCTGGCCTCGAGCCACCAGCTTTCTGGACCTCAGACTCAGAGCCCCTGCCTCA 240

Qy   3016 GGAGACCTGTCTGAGCCAGCACCCTCCTCGAGGAAGGGCT 3075
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Db    241 GGAGACCTGTCTGAGCCAGCACCCTCCTCGAGGAAGGGCT 300

Qy   3076 AGGACTGGCCCGCAGAGCCTGTGCACCAGGCTACCACCACCC 3135
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Db    301 AGGACTGGCCCGCAGAGCCTGTGCACCAGGCTACCACCACCC 360

Qy   3136 CCAGGGTCAGGGGGCCTGCCTTGCCTGGGACCCCACAGCCTGGAGATGGTGCTTATT 3195
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CCAGGGTCAGGGGGCCTGCCTTGCCTGGGACCCCACAGCCTGGAGATGGTGCTTATT 420

Qy   3196 GGCTGCCATGGCTCTGGCACAGTCCAGTGACCCAGGAAGGCACAGGGTCTGA 3252
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCTGCCATGGCTCTGGCACAGTCCAGTGACCCAGGAAGGCACAGGGTCTGA 477
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RESULT 12
BE266788

LOCUS   BE266788   462 bp   mRNA   linear   EST 13-JUL-2000
DEFINITION 601190482F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534309 5',
           mRNA sequence.
ACCESSION BE266788
VERSION   BE266788.1 GI:9140371
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 482)
  AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Plate: LLCM213 row: d column: 22
           High quality sequence stop: 482.
FEATURES   Location/Qualifiers
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                  /mol_type="mRNA"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:3534309"
                  /tissue_type="small cell carcinoma"
                  /cell_line="MGC3"
                  /lab_host="DH10B (phage-resistant)"
                  /clone_lib="NIH_MGC_7"
                  /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                  EcoRI; cDNA made by oligo-dT priming. Directionally
                  cloned into EcoRI/XhoI sites using the following 5'
                  adaptor: GGCACGAG(3). Size-selected >500bp for average
                  insert size 1.8kb. Library constructed by Ling Hong in
                  the laboratory of Gerald M. Rubin (University of
                  California, Berkeley) using ZAP-cDNA synthesis kit
                  (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT   77 a   163 c   155 g   87 t

Query Match   14.5%; Score 470; DB 10; Length 482;
Best Local Similarity 99.8%; Pred. No. 2.3e-78;
Matches 481; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy   2456 ATCTGAGCCCCAGGTAGTAGATGGCATTGAAGACGGCTCGGCTCCGACCAGCCAAGT 2575
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      1 ATCTGAGCCCCAGGGTAGTAGATGGCATTGAAGACGGCTGTGGCTCGGACCAGCCCAAGT  60
Qy   2516 TCTCTTCCGCGTGGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCCTCCCTGGACCAG   2575
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCTCTTCCGCGTGGGCCAGTCTGGCCCGGAATGTAGCAGCAGCCCCTCCCTGGACCAG    120
Qy   2576 AGAGCGGCCTGCTCACTGTTCCCATGGCCGGAGGCAAGGAACACAGACACACTGG     2635
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGAGCGGCCTGCTCACTGTTCCCATGGCCGGAGGCAAGGAACACAGACACACTGG      180
Qy   2636 ACAAGCTTCGGCAGGCGGTGACAGAGCTGTCAGAGCAGGTGCTGCAGATGCGGGAAGGAC  2695
          |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db    181 ACAAGCTTCGGCAGGCCGTGACAGAGCTGTCAGAGCAGGTGCTGCAGATGCGGGAAGGAC   240
Qy   2696 TGCAGTCACTTCGCCAGGCTGTGCAGGTCGCAGCTTGTCTCTGGCGCCCCACAGGGAGGTCC-GTGC  2754
          ||||||||||||||||||||||||||||||||||| |||| |||||||||||||||||||||   ||||
Db    241 TGCAGTCACTTCGCCAGGCTGTGCAGGTCGCAGCTTGTCTCCTGGCGCCCCACAGGGAGGTCC-TGTGC  300
Qy   2755 CCTGGGCATCGGGGAGGAGGGGCCGGCGCCGGCATCCCGTGCCCAGCACCTCCGGGCTTCTGCAGCCTCTG  2814
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTCGGGCATCGGGGAGGAGGGGCCGGCGCCGGCATCCCGTGCCCAGCACCTCCGGGCTTCTGCAGCCTCTG   360
Qy   2815 TGTGTGGACACTGGGGCATCCTCCTACTGCCTGCTCCAGCCCCCAGCTGGCTCTGTGTCTTGAGT  2874
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGTGTGGACACTGGGGCATCCTCCTACTGCCTGCTCCAGCCCCCAGCTGGCTCTGTGTCTTGAGT   420
Qy   2875 GGGACTTGGCCCCACCCTCGTCCGGGGCCTCTCCCTCCCTCGCCCTGCCCTGGGGT  2934
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    421 GGGACTTGGCCCCACCCTCGTCCGGGGCCTCTCCCTCCCTCATGGGCCCTGGGGT   480
Qy   2935 CC  2936
          ||
Db    481 CC  482
```

RESULT 13
AI272282
LOCUS   AI272282   424 bp   mRNA   linear   EST 18-NOV-1998
DEFINITION ap23c04.x1 Schiller oligodendroglioma Homo sapiens cDNA clone
            IMAGE:1956198 3' similar to TR:Q23974 Q23974 PUTATIVE POTASSIUM
            CHANNEL SUBUNIT ;, mRNA sequence.
ACCESSION   AI272282
VERSION   AI272282.1 GI:3894553
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 424)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
            ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
  TITLE   WashU-NCI human EST Project
  JOURNAL   Unpublished
COMMENT   Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Possible reversed clone: similarity on wrong strand
            Possible reversed clone: polyT not found
            Seq primer: -40UP from Gibco
            High quality sequence stop: 401.
FEATURES   Location/Qualifiers
     source 1..424
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:1956198"

            /sex="male"
            /tissue_type="oligodendroglioma"
            /dev_stage="44 years"
            /lab_host="SOLR"
            /clone_lib="Schiller oligodendroglioma"
            /note="Organ: brain; Vector: pBluescript SK- (Stratagene);
            Site_1: EcoRI; Site_2: XhoI; Double-stranded cDNA was
            prepared from human oligodendroglioma using primer
            5'-GAGAGAGAGAGAGAGAGAGAAACTAGTCTGAGT(18)-3'. An EcoRI
            adaptor was used on the 5' end of the cDNA as follows:
            5'-AATTCGGCACGAG-3'. The library was size-selected and
            went through one round of amplification. Average insert
            size is 1.7 kb, with a range from 0.4-12 kb. Tumor
            identification by consensus pathology; contains
            chromosome 1p and 19q deletion as determined by CGH. This
            library was constructed by Dr. Martin Schiller (Johns
            Hopkins University)."
BASE COUNT   82 a   160 c   110 g   72 t
ORIGIN

Query Match   13.0%; Score 424; DB 9; Length 424;
  Best Local Similarity 100.0%; Pred. No. 9.9e-70;
  Matches 424; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   1348 AGGGCCTACATCACCTCCCTCTACTTCGCACTTCGCAGAGCCTCCAGCGTGGCGTTCGGC  1407
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AGGGCCTACATCACCTCCCTCTACTTCGCACTTCGCAGAGCCTCCAGCGTGGCGTTCGGC    60
Qy   1408 AACGTGTCCGCCAACACGGACACCGAGAGACTTCTCCATCTGCACCATGCTCATCGGC   1467
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AACGTGTCCGCCAACACGGACACCGAGAGATCTTCTCCATCTGCACCATGCTCATCGGC   120
Qy   1468 GCCCTGATGCACGGCGGTGGTGTTTGGGAACGTGACGGCCATGTACGCC  1527
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCCTGATGCACGGCGGTGGTGTTTGGGAACGTGACGGCCATCATCCAGCCGCATGTACGCC  180
Qy   1528 CGCGGCTTTCTGTACCACAGCCGCACGCGGACTACTTCCAGCCACTCCGCCATCCACCGI  1587
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CGCGGCTTTCGTTACCACAGCCGCACGCGGACTACTTCCAGCCACTCCGCCATCCACCGI  240
Qy   1588 ATCCCCAAGCCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCACTTCCAGGCCGGTGAAC  1647
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATCCCCAAGCCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCACTTCCAGGCCGGTGAAC  300
Qy   1648 AATGGCATGCAGACACCACCGAGCTGCTGCAGAGGCCTCCCTGACGAGCTCGGCGCGACATC  1707
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AATGGCATGCAGACACCACCGAGCTGCTGCAGAGGCCTCCCTGACGAGCTGCGCGCGAGACATC  360
Qy   1708 GCCATGCACCTGCACAAGGAGGTCCTGCCACTGTTGAGGCCGGCGGCCAGCCGGCGGC  1767
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GCCATGCACCTGCACAAGGAGGTCCTGCCAGCTGCGTTTGAGGCGGCGGCCAGCCGGCGGC  420
Qy   1768 TGCC  1771
          ||||
Db    421 TGCC  424
```

RESULT 14
BQ444229
LOCUS   BQ444229   682 bp   mRNA   linear   EST 29-MAY-2002
DEFINITION UI-M-EXO-bxk-c-05-0-UI.r1 NIH_BMAP_EXO Mus musculus cDNA clone
            IMAGE:5709244 5', mRNA sequence.
ACCESSION   BQ444229
VERSION   BQ444229.1 GI:21247341
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 682)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished

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Qy   1750  GAGGCGGCCAGCCGCGGGCTGCCTGGGGCACTGTCTCTGGGCCCCGCCTTCTGC 1809
           | |||| ||| |||||||||| ||||||||||| || ||| || ||||||||
Db    523  GGAGCGGCTAGCAAGGGCTGCCTGCGGGCCCTCTCCTTGCACATCAAGACCTCCTTCTGT 582

Qy   1810  ACGGCCGGCGGAGTACCTCATCCACCAAGGCGATGCCCTGCAGCGCCTCTACTTTGTCTGC 1869
           | || ||| ||||||||| | || |||||||||| ||||||| |||||| ||||
Db    583  GCTCTCGGGAGTACCTGTTACGCCGGGGGATGCCTCCAGGCACACTACTACCGTCTGC 642

Qy   1870  TCTGGCTCCATGGAGGTGCTCAAGG 1894
           ||||||| |||||| ||||||| ||
Db    643  TCTGGCTCCTGAGGTGCTCCGGG 667

RESULT 15
BI975332
LOCUS       BI975332            522 bp   mRNA    linear   EST 23-OCT-2001
DEFINITION  483675 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BI975332
VERSION     BI975332.1  GI:16349737
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 522)
AUTHORS     Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
TITLE       Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
JOURNAL     Genome Res. 11 (4), 626-630 (2001)
MEDLINE     21180013
PUBMED      11282978
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the 'minscore 18
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 108  row: C  column: 22
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES            Location/Qualifiers
     source        1..522
                   /organism="Bos taurus"
                   /mol_type="mRNA"
                   /db_xref="taxon:9913"
                   /tissue_type="pooled"
                   /lab_host="DHI0B"
                   /clone_lib="MARC 2BOV"
                   /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                   Library made from pooled tissue from testis, thymus,
                   semitendonosus muscle, longissimus muscle, pancreas,
                   adrenal, and endometrium."
BASE COUNT    80 a    200 c    148 g    94 t
ORIGIN

Query Match      11.1%;  Score 361;  DB 12;  Length 522;
Best Local Similarity   89.4%;  Pred. No. 7.3e-58;
Matches   412;  Conservative  0;  Mismatches  45;  Indels  4;  Gaps  2;

Qy   2792  CCTCCGGGTTCTGCAGCCTCGTCTGTGTGGACACTGGGCATCCTCCTACTGCCTGCAGC 2851
           ||||||||  || || ||||| || |||||||||||||| ||||||||||||||
Db      4  CCTCTGGCTGCTGCAGCCCCTGTGTGTGGACACTGGGCATCCTCCTGCTGCCTACAGC 63
```

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Qy   1750  GAGGCGGCCAGCCGCGGGCTGCCTGGGGCACTGTCTCTGGGCCCCGCCTTCTGC 1809
Db    523  GGAGCGGCTAGCAAGGGCTGCCTGCGGGCCCTCTCCTTGCACATCAAGACCTCCTTCTGT 582
```

COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue procurement: Dr James Lin, University of Iowa
           cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
           cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
           DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
           Clone Distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           This clone was contributed by the Brain Molecular Anatomy Project
           (BMAP)
FEATURES   Seq primer: pYX-5.
           Location/Qualifiers
     source   1..682
                   /organism="Mus musculus"
                   /mol_type="mRNA"
                   /strain="C57BL/6"
                   /db_xref="taxon:10090"
                   /clone="IMAGE:5709244"
                   /tissue_type="whole brain"
                   /dev_stage="embryo 15.5 dpc"
                   /lab_host="DHI0B (T1 phage resistant)"
                   /clone_lib="NIH_BMAP_EX0"
                   /note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
                   Site_2: Not I: The library was constructed according to
                   Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                   1996. Denatured mRNA was size fractionated on a 1% agarose
                   gel. First strand cDNA synthesis was primed with an
                   oligo-dT primer containing a Not I site. Double stranded
                   cDNA was size selected according to mRNA size fraction,
                   ligated with EcoR I adaptor, digested with Not I, and then
                   cloned directionally into pYX-Asc vector. The library tag
                   sequence located between the Not I site and the polyA tail
                   is GTGCGTGGAA. This library was created for the
                   University of Iowa Mouse Brain Molecular Anatomy Project
                   (BMAP): 'Gene Discovery in the Developing Mouse Nervous
                   System', supported by National Institutes of Mental Health
                   (NIMH), Hemin Chin, Ph.D., Program coordinator."
BASE COUNT   128 a   205 c   202 g   147 t
ORIGIN

Query Match   11.4%; Score 369.8; DB 13; Length 682;
Best Local Similarity   78.4%; Pred. No. 1.7e-59;
Matches   443; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

Qy   1330 GGCGGCCCGTGCTGCCAGCGCCTCACATCACCTCCCTCTACTTCGCACTCAGCAGCCTC 1389
           || || ||| ||||| |||||| ||| | | | ||||| ||| |||||||||||
Db   103 GGTGGACCATCCGGGCGAGTGCCTACATGCCTCTGCTACTTCACGCTGAGCAGCCTC 162

Qy   1390 ACCAGCGTGGGCTTCGGCAACGTGTCCGGCAACACGGACACCGAGAAGATCTTCTCCATC 1449
           ||| ||||| ||||| ||||||| | | ||||| |||| || || |||||||||||
Db   163 ACCAGTGTAGGCTTCGGCAACGTGTGTGCAACACAGACGCTGAGAAGATCTTCTCCATC 222

Qy   1450 TGCACCATGCTCATCGGCGCCCTGATCGACGCGGTGGTGTTTGGGAACGTGACGGCCATC 1509
           |||||||| |||| |||| |||||| || || ||| ||||||| ||||| || | |||
Db   223 TGCACGATGCTCATAGGCGCGCTGATCGACGCGGTGGTGTTTGGGAATGTCACAGCCATC 282

Qy   1510 ATCCACGCCATGTACGGCCCGCGCCTTTCGTACCACAGCGCACGCGGGACCTGGCGGAC 1569
           ||||||||||||| |||| ||||||| |||||||||||||| || || | ||| ||
Db   283 ATCCACGCCATGTACTCCGGCAGCTCGGCTCTACCACCACCAGCGCCATGAAGGATCTCAAGGAC 342

Qy   1570 TACATCCGCATCCACCGTATCCCGCCCCCACTCAAGCAGCCCATGCTGGACTACTTCCAG 1629
           | |||||||| || || ||| || | || |||||||| ||||||||||||||| |||
Db   343 TTCATCCGAGTCCAGTCGCATCCCGCCCCCACTCAAGCAGCCCATCGTCGACTACTTCCAG 402

Qy   1630 GCCACCTGGGCCGGTGAACAATGGCATCGACACCACCGACGTCGTGCAGAGCCTCCCTGAC 1689
           ||||| |||||| || |||| || |||| |||||| || ||||| ||||| |||| |||
Db   403 ACGACGTGGGCAGTCAACAGCGGCCATCGATCGATGCCAACAGTTACTGCGTGACTTCCCGGAT 462

Qy   1690 GAGCTGCGCGGACGCAGAGAACATCGCCATCCACCTGCACACGAGGAGGTCCACAGAGG 1749
           ||||||| || | | ||| | | || || || | |||| | |||||||||||
Db   463 GAGCTGCGTGCTGCTCATGCCATGCCATGTTGCACCTGAACACGGAGATCCTGAGCTGCACACGTCCTGCTCTGTTT 522
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Qy   2852  CCCCAGCTGGCTCTGTCTTGAGTGGGACTTGGCCCCACCCTCGGGGGCTCCTCCCC 2911
           || | ||||||||||||||||||||||||||||| |||||||||||||||| ||:|||| ||:|||||
Db     64  CCTCAGCTGGCTCTGTCTTGAGTGGGACCTGGCCCCCACCCTCGTCCAGGGCCCCCCTCCC :23

Qy   2912  TCATGGCACCCTGGCCCTGGGGTCCCCAGCGTCTCAGAGCTCCCCTGGCCTCGAGCCA 2971
           ||||||| ||||||||| ||| |||| || |||||||||| || ||||||||:|||||:
Db    124  TCATGGCTCCCTGGCCCTGGGGCCCCCTGCATCTCAGAGCTCACCATGGCCTCGAGCCA 183

Qy   2972  CAGCTTTCTGGACCTCCACCTCAGACTCAGAGCCCCTGCCTCAGGAGACTCCGCTCTG 3032
           | ||||| ||||||||:||| :|||| | ||||||| | |::|||:||| ||||| |:
Db    184  CTGCTTTTTGGACCTCCACCTCTGACTCGGGAGCCCCCAGGCTCAGGAGAACTCGCCCTG 243

Qy   3032  AGCCCAGCACACCCCTGCCTCCCCTCCTTCTGAGGAAGGGCTAGGACTGGGCCCGCAG 3092
           |||||||||||||||||| |||||||||| | ||||  - | ||||||||||||||:| ||
Db    244  AGCCCAGCACCCCCTGGCTTACCGCCTC---CCGAGGAAGGGCTAGGACTGGGCCCCCGG 300

Qy   3092  AGCCTGTGAGCCAGGCTACCAGCACTGGAGAGCCCCCACCAGGGTCAGGGGGCC 3151
           |||| |||:|||||||||||||||||||| ||||||||||||| || :|||||||
Db    301  AGCCCATGACCCCAGGCTGAGGCTGCCAGCACCGGAGAGCCCCCACCAGCTTCGGGGGGCC 360

Qy   3152  TGGCCTTGCCCTGGGACCCCACAGCCTGGAGATGGTGCTTATTGGCTGCCATGGCTCTG 3211
           ||||||||||||| |||| |||||||| ||||||:||||| ||||||| ||||||
Db    361  ACGCCTTGCCCTGGGAGCCCCATAGCCTGGAGATGGTGCTTATCGGCTGCCACGGCTCTG 420

Qy   3212  GCACAGTCCAGTGGACCCAGGAAGGAAGGCACAGGGTCTGA 3252
           | - ||||||||||| ||||||||:|||||||||||||||||
Db    421  GTACAGTCCAGTGGACCCAGGAAGAA-GCACAGGGGTCTGA 460
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Search completed: October 1, 2003, 21:12:57
Job time :5973 secs